

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 15, 2003, 08:32:08 ; Search time 70 Seconds

(without alignments)  
344.548 Million cell updates/sec

Title: US-09-937-555A-2

Sequence: 1 ESDYSLCQGRKELDDDMHEM.....DYGAGYTCDDMNLCTGH 181

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	997	100.0	181	21	AA19333
2	333	32.4	238	20	AA123611
3	319	32.0	248	20	AA123609
4	306.5	30.7	241	20	AA123610
5	302.5	30.0	274	20	AA123604
6	298	29.9	231	14	AA123595
7	296.3	29.7	267	20	AA123605
8	296.3	29.7	270	20	AA123603
9	296.3	29.7	270	20	AA123603
10	290.5	29.1	232	20	AA123593

11	290	29.1	257	23	AA120891	Ancylostoma caninum
12	290	29.1	272	20	AA123606	Canine hookworm ne
13	290	29.1	274	20	AA124288	Canine hookworm ne
14	290	29.1	274	20	AA123600	Canine hookworm ne
15	290	29.1	274	20	AA123601	Canine hookworm ne
16	290	29.1	274	20	AA123592	Canine hookworm ne
17	290	29.1	274	20	AA123591	Canine hookworm ne
18	290	29.1	274	23	AA123599	Neutrophil inhibi
19	290	29.1	274	23	AA123599	Canine hookworm ne
20	290	29.1	274	23	AA123599	Canine hookworm ne
21	287	28.8	274	20	AA123599	Canine hookworm ne
22	286.5	28.5	234	14	AA123607	Canine hookworm ne
23	284.5	28.5	270	20	AA123608	Canine hookworm ne
24	269	27.0	263	20	AA123602	Canine hookworm ne
25	266	26.7	224	14	AA123598	Canine hookworm ne
26	266	26.7	224	14	AA123598	Canine hookworm ne
27	265.5	26.6	424	17	AA123595	Canine hookworm ne
28	262	26.3	218	17	AA123592	Canine hookworm ne
29	260	26.1	218	17	AA123592	Canine hookworm ne
30	255.5	25.6	192	22	AA123590	Canine hookworm ne
31	255	25.6	208	14	AA123594	Canine hookworm ne
32	255	25.6	208	20	AA123594	Canine hookworm ne
33	214	21.5	222	19	AA123594	Canine hookworm ne
34	205	20.6	454	13	AA123594	Canine hookworm ne
35	201	20.2	440	13	AA123594	Canine hookworm ne
36	200	20.1	189	14	AA123590	Canine hookworm ne
37	200	20.1	189	14	AA123590	Canine hookworm ne
38	190	19.1	253	22	AA123590	Canine hookworm ne
39	187	18.8	220	22	AA123590	Canine hookworm ne
40	161.5	16.2	223	22	AA123590	Canine hookworm ne
41	160	16.0	300	22	AA123590	Canine hookworm ne
42	159	15.9	262	22	AA123590	Canine hookworm ne
43	159	15.9	262	22	AA123590	Canine hookworm ne
44	159	15.9	262	22	AA123590	Canine hookworm ne
45	159	15.9	262	22	AA123590	Canine hookworm ne

#### ALIGNMENTS

```

RESULT 1
ID AA19333 standard; Protein; 181 AA.
AA19333
AC AA19333;
DE 19-FEB-2001 (first entry)
XX
XX A hookworm platelet inhibitor polypeptide.
XX
XX Hookworm platelet inhibitor; platelet aggregation; fibrinogen; collagen;
XX platelet function; cancer; myocardial infarction; unstable angina;
XX stroke; arterial angioplasty; thrombocytopenic purpura; malaria;
XX hemolytic uremic syndrome; heparin-induced thrombosis; vaccine.
XX
XX Ancylostoma caninum.
XX
XX WO200058341-A1.
XX
XX 05-OCT-2000.
XX
XX 30-MAR-2000; 2000MO-US08519.
XX
XX 31-MAR-1999; 99US-0127239.
XX
XX (UYVA ) UNIV YALE.
XX
XX Cappello M, Chadderton RC, Del Valle A, Harrison LM;
XX WPI: 2000-672551/65.
XX N-PSDB; AA175986.
XX
XX Novel platelet inhibitor from hookworms useful for veterinary and

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PT medical purposes in cancer therapy, block platelet aggregation by  
 PT interfering with binding of cell surface integrin with its respective  
 PT ligand  
 XX  
 XX  
 PS Claim 1; Page 36; 38pp; English.

CC The present sequence represents a hookworm platelet inhibitor polypeptide  
 CC of *Ancylostoma caninum* the hookworm platelet inhibitor not only blocks  
 CC platelet aggregation, but also prevents adhesion of platelets to  
 CC fibrinogen and possibly also collagen. In vitro, the inhibitor inhibits  
 CC fibrinogen binding to GPIIb/IIIa. The polypeptides and polynucleotides  
 CC are useful for inhibiting platelet function. Thus the polypeptides are  
 CC useful for veterinary and medical purposes in vascular biology and cancer  
 CC therapy and may also be useful for treating myocardial infarction,  
 CC unstable angina, stroke, cerebral and peripheral arterial angioplasty,  
 CC thrombocytopenic purpura/hemolytic uremic syndrome, heparin-induced  
 CC thrombosis, microvascular and cerebral malaria. They are also useful  
 CC for treating variety of cancers by altering the neoplastic state of  
 CC tumor cells, repressing gene induction and inhibiting cancer cell  
 CC migration on extracellular matrix substances and invasion of distant  
 CC tissues. The polypeptides are also useful as vaccines for reducing the  
 CC burden of hookworm infections in population at risk.

CC Sequence 181 AA:

SO  
 Query Match 100.0%; Score 997; DB 21; Length 181;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-95;  
 Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 EGDYSLCOOREKLDMDREMFTELHNGYRAAARVYKSKKATMYDCTLEKAYSKAEK 60  
 DB 1 EGDYSLCOOREKLDMDREMFTELHNGYRAAARVYKSKKATMYDCTLEKAYSKAEK 60  
 DB 61 CSEPESESEENVDFSAATINIPLEAGNSMWEIPELNGKVNKNTSINANVWDSHD 120  
 DB 61 CSEPESESEENVDFSAATINIPLEAGNSMWEIPELNGKVNKNTSINANVWDSHD 120  
 OY 121 KLGCAVYVDCSGKTHVCOYGPBKAQKGTIYEGAPGRCSDGAGVTCDDDMONLIG 180  
 DB 121 KLGCAVYVDCSGKTHVCOYGPBKAQKGTIYEGAPGRCSDGAGVTCDDDMONLIG 180  
 OY 181 H 181  
 DB 181 H 181

RESULT 2  
 ID AAY23611 standard; Protein: 238 AA.  
 XX  
 AC AAY23611;  
 DT 03-SEP-1999 (first entry)  
 DE Neutrophil inhibitory factor (AcenIF3).  
 XX  
 KW Neutrophil inhibitory factor; NIF; mutant; shock; stroke;  
 KW allograft rejection; vasculitis; autoimmune diabetes; ARDS;  
 KW rheumatoid arthritis; inflammatory skin disease; myocardial infarction;  
 KW inflammatory bowel disease; adult respiratory distress syndrome;  
 KW ischemia-reperfusion injury; acute inflammation; bacterial infection;  
 KW vaccine; parasitic worm infection; antihelminic.  
 XX  
 AC Ancylostoma ceylanicum.  
 OS  
 XX US5919900-A.  
 PN  
 XX 06-JUL-1999.  
 PD  
 XX 26-MAY-1995; 95US-0450497.  
 PF  
 XX 23-DEC-1993; 93US-0173510.  
 PR  
 XX 11-MAY-1992; 92US-0881721.  
 PR

PR 24-DEC-1992; 92US-0996972.  
 PR 11-MAY-1993; 93US-0060433.  
 PR 10-NOV-1993; 93US-0151064.  
 PR 26-MAY-1995; 95US-0450497.  
 XX  
 XX  
 PA (CORV-) CORVAS INT INC.  
 PI Foster DL, Moyle M;  
 XX  
 XX WPI: 1999-403975/34.  
 DR N-PSDB: AAX85548.  
 XX  
 XX  
 PT Mutant Neutrophil Inhibitory Factors useful for treating  
 PT inflammatory conditions and especially to prevent or decrease  
 PT inflammatory responses  
 PS  
 PS Example 22; Fig 9A-B; 13pp; English.

CC The specification describes mutant Neutrophil Inhibitory Factors (NIFs),  
 CC where at least 1 of the Asp residues at positions 18, 87, 110, 130, 137,  
 CC or 223 in the wild type sequence (see AAY23591) is replaced by a Gln  
 CC residue. NIFs may be useful for treating shock, stroke, acute and  
 CC chronic allograft rejection, vasculitis, autoimmune diabetes, rheumatoid  
 CC arthritis, inflammatory skin diseases, inflammatory bowel disease, adult  
 CC respiratory distress syndrome (ARDS), ischemia-reperfusion injury  
 CC following myocardial infarction, and acute inflammation caused by  
 CC bacterial infection such as sepsis or bacterial meningitis. NIFs or NIF  
 CC fragments may be used as vaccines against parasitic worm infection.  
 CC Anti-NIF antibodies may be useful for detecting infection of a mammalian  
 CC host by a parasitic worm, as antihelminic agents, and in the detection  
 CC and isolation of NIF from tissue homogenates, cloned cells etc. NIFs may  
 CC be useful for the detection of NIF mimics or antagonists in other  
 CC compounds. Other NIF agonists and inhibitors may also be used as  
 CC antihelminic agents. The present sequence represents a hookworm NIF.

SO Sequence 238 AA:

Query Match 32.4%; Score 323; DB 20; Length 238;  
 Best Local Similarity 36.2%; Pred. No. 3.5e-25;  
 Matches 75; Conservative 31; Mismatches 67; Indels 34; Gaps 8;

OY 1 EGDYSLCOORE-KLDDMDREMFTELHNGYRA-----AFANRYSKMTFM 44  
 DB 10 KGDPECKKONGSKMNEARRRFLHNGYRSIALGHVNISESENEFTLAHAKSMRL 69  
 OY 45 VYDCTLEKAYSKA-EKCEPESESE---EENVDFSAATINIPLEAGNSMWEIPEL 97  
 DB 70 DYDGDAGSKYSEAIKQCSSKSSSAEDENYVIDNTYEDVDPAKAISSWTQARNL 129  
 OY 98 ----RGVYKAKGKTSINANVWDSHDKGCAVDC--SGKTHVCOYGPBKAQKGTIY 151  
 DB 130 THAEGIFPYOMDSVSDRANVAMPAREKLGCAVTCDDGNTTHVCHGKAKNTEPIY 189  
 OY 152 EEGAPGRCSDGAGVTCDDDMONLIG 178  
 DB 190 KVGVPSCNCTEYTRG-----DEKVPFC 211

RESULT 3  
 ID AAY23609 standard; Protein: 248 AA.  
 XX  
 AC AAY23609;  
 DT 03-SEP-1999 (first entry)  
 DE Canine hookworm neutrophil inhibitory factor AcanNIF9 polypeptide.  
 XX  
 KW Neutrophil inhibitory factor; NIF; mutant; shock; stroke;  
 KW allograft rejection; vasculitis; autoimmune diabetes; ARDS;  
 KW rheumatoid arthritis; inflammatory skin disease; myocardial infarction;  
 KW inflammatory bowel disease; adult respiratory distress syndrome;  
 KW ischemia-reperfusion injury; acute inflammation; bacterial infection;  
 KW

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XX vaccine: parasitic worm infection: antihelminic.
XX
OS Ancylostoma caninum.
XX
PN US5919900-A.
XX
PD 06-JUL-1999.
XX
PF 26-MAY-1995; 950S-0450497.
XX
PR 23-DEC-1993; 930S-0173510.
PR 11-MAY-1992; 920S-0881721.
PR 24-DEC-1992; 920S-0996972.
PR 11-MAY-1993; 930S-0060433.
PR 10-NOV-1993; 930S-0151064.
PR 26-MAY-1995; 950S-0450497.
XX
PA (CORV-) CORVAS INT INC.
XX
PI Foster DL, Moyle M;
XX
DR WPI; 1999-403975/34.
XX
DR N-PSDB; AAX85546.
XX
PT Mutant Neutrophil Inhibitory Factors useful for treating
PT inflammatory conditions and especially to prevent or decrease
PT inflammatory responses
XX
PS Example 21; Fig 16A-V; 131pp; English.
XX
XX The specification describes mutant Neutrophil Inhibitory Factors (NIFs),
XX where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197,
XX or 223 in the wild type sequence (see MAY23591) is replaced by a Gln
XX residue. NIFs may be useful for treating shock, stroke, acute and
XX chronic allograft rejection, vasculitis, autoimmune diabetes, rheumatoid
XX arthritis, inflammatory skin diseases, inflammatory bowel disease, adult
XX respiratory distress syndrome (ARDS), ischemia-reperfusion injury
XX following myocardial infarction, and acute inflammation caused by
XX bacterial infection such as sepsis or bacterial meningitis. NIFs or NIF
XX fragments may be used as vaccines against parasitic worm infection.
XX Anti-NIF antibodies may be useful for detecting infection of a mammalian
XX host by a parasitic worm, as antihelminic agents, and in the detection
XX and isolation of NIF from tissue homogenates, cloned cells etc. NIFs may
XX be useful for the detection of NIF mutants or antagonists in other
XX compounds. Other NIF agonists and inhibitors may also be used as
XX antihelminic agents. MAY23600-10 represent canine hookworm NIF proteins.
XX
XX Sequence 248 AA:
XX
Query Match 32.08; Score 319; DB 20; Length 248;
Best Local Similarity 38.58; Pred. No. 9.6e-25;
Matches 79; Conservative 18; Mismatches 64; Indels 44; Gaps 7;
XX
QY 7 COQRE-----KLDDMKEMFTELHNGYRAFAFARNY-----KTSKMR 42
DB 23 CPQNEVENEKGFDDAMKLFALHNGYRSKIALGHVSITESEEDYDLYDLAFTASKMR 82
QY 43 TMYVDTLEEKAYKSAEKSEPSSE---EENV-----DVSAAATNIPLENGSNMS 92
DB 83 YLEVDCEAKSAYESAKKQTTAFSTKYDENLQVIEDPDINHAA-----LKAIISMAF 137
QY 93 ELFEF---RQKYVNRKNGTSNIAMVDSHDKLGCAYVDC-SGTHVYVQGYGEAKGOG 147
DB 138 EAFNINLKTGEGVYRSLINISNFMILAMDTRHEKVGCAVYKCSGTHVYVCHPIYAKKES 197
QY 148 KTIYEGAPCSRCSYDGAGVTCDD 172
DB 198 KPIYSIGMPCRGNDYASKFCFCHAD 222

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XX
XX AAY23610;
XX
AC 03-SEP-1999 (first entry)
XX
DT Canine hookworm neutrophil inhibitory factor AcanNIF18 polypeptide.
XX
DE Neutrophil Inhibitory factor; NIF; mutant; shock; stroke;
XX
KW allograft rejection; vasculitis; autoimmune diabetes; ARDS;
KW rheumatoid arthritis; inflammatory skin disease; myocardial infarction;
KW inflammatory bowel disease; adult respiratory distress syndrome;
KW ischemia-reperfusion injury; acute inflammation; bacterial infection;
XX vaccine; parasitic worm infection; antihelminic.
XX
OS Ancylostoma caninum.
XX
PN US5919900-A.
XX
PD 06-JUL-1999.
XX
PF 26-MAY-1995; 950S-0450497.
XX
PR 23-DEC-1993; 930S-0173510.
PR 11-MAY-1992; 920S-0881721.
PR 24-DEC-1992; 920S-0996972.
PR 11-MAY-1993; 930S-0060433.
PR 10-NOV-1993; 930S-0151064.
PR 26-MAY-1995; 950S-0450497.
XX
PA (CORV-) CORVAS INT INC.
XX
PI Foster DL, Moyle M;
XX
DR WPI; 1999-403975/34.
XX
DR N-PSDB; AAX85547.
XX
PT Mutant Neutrophil Inhibitory Factors useful for treating
PT inflammatory conditions and especially to prevent or decrease
PT inflammatory responses
XX
PS Example 21; Fig 16A-V; 131pp; English.
XX
XX The specification describes mutant Neutrophil Inhibitory Factors (NIFs),
XX where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197,
XX or 223 in the wild type sequence (see MAY23591) is replaced by a Gln
XX residue. NIFs may be useful for treating shock, stroke, acute and
XX chronic allograft rejection, vasculitis, autoimmune diabetes, rheumatoid
XX arthritis, inflammatory skin diseases, inflammatory bowel disease, adult
XX respiratory distress syndrome (ARDS), ischemia-reperfusion injury
XX following myocardial infarction, and acute inflammation caused by
XX bacterial infection such as sepsis or bacterial meningitis. NIFs or NIF
XX fragments may be used as vaccines against parasitic worm infection.
XX Anti-NIF antibodies may be useful for detecting infection of a mammalian
XX host by a parasitic worm, as antihelminic agents, and in the detection
XX and isolation of NIF from tissue homogenates, cloned cells etc. NIFs may
XX be useful for the detection of NIF mutants or antagonists in other
XX compounds. Other NIF agonists and inhibitors may also be used as
XX antihelminic agents. MAY23600-10 represent canine hookworm NIF proteins.
XX
XX Sequence 241 AA:
XX
Query Match 30.78; Score 306.5; DB 20; Length 241;
Best Local Similarity 38.18; Pred. No. 1.8e-23;
Matches 80; Conservative 19; Mismatches 68; Indels 43; Gaps 7;
XX
QY 1 EGDYSLCOQREKL---DDDKREMFTELHNGYRAFAFARNY-----K 37
DB 11 EHDPTCPONGERMEKGFDDAMKLFALHNGYRSRSLALGHVSITESEEDYDLYDLAFT 70
QY 38 TSKMRTMYDCTLEEKAYKSAEKSEPSSE---EENV-----DVSAAATNIPLENG 87
DB 71 ASKMRILYDCEAKSAYESAKKQTTAFSTKYDENLQVIEDPDINHAA-----LKAI 125

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QY 88 NSWMSIFEL-----RGKYNNKNGKTSNIAMVWSDHRLGCAVDCSGK-THVCOYGP 142  
 Db 126 ISWATAFNLNKTGCGVYRSIINISNFANLAMDTRERFGCAVDCSPRTTHVCHYK 185  
 QY 143 AKGDGTYIEEGAPCSRCSDGAGVCCDD 172  
 Db 186 VEREGKPIYTTGVPICGCGSYANRPFCHAD 215

RESULT 5  
 AAY23604  
 ID AAY23604 standard; Protein; 274 AA.  
 AC AAY23604;  
 XX  
 DT 03-SEP-1999 (first entry)  
 DE Canine hookworm neutrophil inhibitory factor Acanif4 polypeptide.  
 XX  
 KW Neutrophil inhibitory factor; NIF; mutant; shock; stroke;  
 KW allograft rejection; vasculitis; autoimmune diabetes; ARDS;  
 KW rheumatoid arthritis; inflammatory skin disease; myocardial infarction;  
 KW inflammatory bowel disease; adult respiratory distress syndrome;  
 KW ischemia-reperfusion injury; acute inflammation; bacterial infection;  
 KW vaccine; parasitic worm infection; antihelminic.  
 OS Ancylostoma caninum.  
 XX  
 FN US5919900-A.  
 XX  
 PD 06-JUL-1999.  
 XX  
 PF 26-MAY-1995; 95US-0450497.  
 XX  
 PR 23-DEC-1993; 93US-0173510.  
 PR 11-MAY-1992; 92US-0881721.  
 PR 24-DEC-1992; 92US-0996972.  
 PR 11-MAY-1993; 93US-0060433.  
 PR 10-NOV-1993; 93US-0151064.  
 PR 26-MAY-1995; 95US-0450497.  
 XX  
 PA (CORV-) CORVAS INT INC.  
 XX  
 PI Foster DL, Moyle M;  
 XX  
 DR WPI: 1999-403975/34.  
 DR N-PSDB: AAX85541.  
 XX  
 PT Mutant Neutrophil Inhibitory Factors useful for treating  
 PT inflammatory conditions and especially to prevent or decrease  
 PT inflammatory responses  
 XX  
 PS Example 21; Fig 16A-V; 131pp; English.  
 XX  
 CC The specification describes mutant Neutrophil Inhibitory Factors (NIFs),  
 CC where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197,  
 CC or 223 in the wild type sequence (see AAY23591) is replaced by a Gln  
 CC residue. NIFs may be useful for treating shock, stroke, acute and  
 CC chronic allograft rejection, vasculitis, autoimmune diabetes, rheumatoid  
 CC arthritis, inflammatory skin diseases, inflammatory bowel disease, adult  
 CC respiratory distress syndrome (ARDS), ischemia-reperfusion injury  
 CC following myocardial infarction, and acute inflammation caused by  
 CC bacterial infection such as sepsis or bacterial meningitis. NIFs or NIF  
 CC fragments may be used as vaccines against parasitic worm infection.  
 CC Anti-NIF antibodies may be used for detecting infection of a mammalian  
 CC host by a parasitic worm, as antihelminic agents, and in the detection  
 CC and isolation of NIF from tissue homogenates, cloned cells etc. NIFs may  
 CC be useful for the detection of NIF mimics or antagonists in other  
 CC compounds. Other NIF agonists and inhibitors may also be used as  
 CC antihelminic agents. AAY23600-10 represent canine hookworm NIF proteins.  
 CC  
 XX Sequence 274 AA;

Query Match 30.5%; Score 304.5; Db 20; Length 274;  
 Best Local Similarity 32.6%; Pred. No. 3.5e-23;  
 Matches 76; Conservative 24; Mismatches 66; Indels 67; Gaps 9;

QY 6 LCOOGRK-----LDDDRKEMFTELHNGYRAAFARNY----- 36  
 Db 20 MCKRRTMVPDGFNDLSRLQFLAMHNGYRSLLALGAVGISKOPIDDDYDDYFYFSSYA 79  
 QY 37 -KTSKRTMYDCDTELEKAYKSAEK---SEEPSSEENVDFSAATINI---PLEGNS 89  
 Db 80 PRASKMYLEIDCEDEAKSAYVASKSNISSPGEGYDENKRYIFENS-NISEALKAMIS 138  
 QY 90 WMSSEIFEL-----RGKYNNKNGKTSNIAMVWSDHRLGCAVDC-----SGK 132  
 Db 139 WAKKAFNLNKTGCGVYRSIINISNFANLAMDTRERFGCAVDCPLGEIDTTSNDD 198  
 QY 133 T-----HYVCOYGPPEAKGPKTYIEEGAPCSRCSDGAGV-----TCDD 172  
 Db 199 TYAVAHVCHYPRKLEKEKQIYEVGKPCDRCSEYSKANNITSPMNVCMND 251

RESULT 6  
 AAY23595  
 ID AAY23595 standard; Protein; 231 AA.  
 AC AAY23595;  
 XX  
 DT 03-SEP-1999 (first entry)  
 DE Canine hookworm neutrophil inhibitory factor isoform clone 3FL.  
 XX  
 KW Neutrophil inhibitory factor; NIF; mutant; shock; stroke;  
 KW allograft rejection; vasculitis; autoimmune diabetes; ARDS;  
 KW rheumatoid arthritis; inflammatory skin disease; myocardial infarction;  
 KW inflammatory bowel disease; adult respiratory distress syndrome;  
 KW ischemia-reperfusion injury; acute inflammation; bacterial infection;  
 KW vaccine; parasitic worm infection; antihelminic.  
 OS Ancylostoma caninum.  
 XX  
 FN US5919900-A.  
 XX  
 PD 06-JUL-1999.  
 XX  
 PF 26-MAY-1995; 95US-0450497.  
 XX  
 PR 23-DEC-1993; 93US-0173510.  
 PR 11-MAY-1992; 92US-0881721.  
 PR 24-DEC-1992; 92US-0996972.  
 PR 11-MAY-1993; 93US-0060433.  
 PR 10-NOV-1993; 93US-0151064.  
 PR 26-MAY-1995; 95US-0450497.  
 XX  
 PA (CORV-) CORVAS INT INC.  
 XX  
 PI Foster DL, Moyle M;  
 XX  
 DR WPI: 1999-403975/34.  
 XX  
 PT Mutant Neutrophil Inhibitory Factors useful for treating  
 PT inflammatory conditions and especially to prevent or decrease  
 PT inflammatory responses  
 XX  
 PS Example 10; Fig 9A-E; 131pp; English.  
 XX  
 CC The specification describes mutant Neutrophil Inhibitory Factors (NIFs),  
 CC where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197,  
 CC or 223 in the wild type sequence (see AAY23591) is replaced by a Gln  
 CC residue. NIFs may be useful for treating shock, stroke, acute and  
 CC chronic allograft rejection, vasculitis, autoimmune diabetes, rheumatoid  
 CC arthritis, inflammatory skin diseases, inflammatory bowel disease, adult  
 CC respiratory distress syndrome (ARDS), ischemia-reperfusion injury  
 CC following myocardial infarction, and acute inflammation caused by



CC bacterial infection such as sepsis or bacterial meningitis. NIFs or NIF  
CC fragments may be used as vaccines against parasitic worm infection  
CC Anti-NIF antibodies may be useful for detecting infection of a mammalian  
CC host by a parasitic worm, as antihelminthic agents, and in the detection  
CC and isolation of NIF from tissue homogenates, cloned cells etc. NIFs may  
CC be useful for the detection of NIF mimics or antagonists in other  
CC compounds. Other NIF agonists and inhibitors may also be used as  
CC antihelminthic agents. AAY23592-98 represent isoform clones of canine  
CC hookworm NIF.

SO Sequence 231 AA;

Query Match 30.0%; Score 299; DB 20; Length 231;  
Best Local Similarity 35.7%; Pred. No. 1e-22;

Matches 74; Conservative 20; Mismatches 58; Indels 58; Gaps 8;

OY 6 LCQOREK---LDDMRKEMTEELNGYRAAFARNY----- 36  
DB 16 ICSQNGTGMEFGFNDMSRLKFLKLEMHNGYRSLALGHISITEPEESYDDDDGYGEVLAP 75  
OY 37 KTSKMRMYDCTLEEKAYKSAKSCSEPSSE-----EENVDFSAATLNIPLA 86  
DB 76 SASKRRMYEYDCEAEKSAKSAKSCSDSSSPGEGYDENKYLENSNISERARLAI----- 131  
OY 87 GNSWSEIFEL---RGKYNNKNGKTSNIANWVDSHDKIGCAVYDCSGK-----THYV 136  
DB 132 -LSWAKKAFDLNKTGEGVLYRSNLTISNFANLAMDREKFGCAVAKCPLEDTSATTHYV 190  
OY 137 COYGEPAK---DGKTIYEGAPCSRCSY 163  
DB 191 CHY-PKIEGEKEKQIYKVGTPCGDCSEY 219

RESULT 7

AAR52987  
ID AAR52987 standard; Protein: 231 AA.

AC AAR52987;

DT 02-JUN-1994 (first entry)

DE Canine hookworm Neutrophil Inhibitory Factor isoform 2FL.

KW neutrophil inhibitory factor; NIF; glycoprotein; endoparasite;

KM nematode; parasitic worm; canine hookworm; peritoneal inflammation.

OS Ancylostoma caninum.

PN WO9323063-A.

PD 25-NOV-1993.

PE 11-MAY-1993; 93MO-US04502.

PR 11-MAY-1992; 92US-0881721.

PR 24-DEC-1992; 92US-0996972.

PA (CORV-) CORVAS INT INC.

PI Foster DL, Moyle M, Vlasuk GP;

PI 1993-386208/48.

PT New neutrophil inhibitory factor from parasitic worms - for

PT preventing and treating inflammation, also derived nucleic acid,

PT vectors, transformed hosts and antibodies

PS Example 10; Fig 9; 114pp; English.

CC A canine hookworm cDNA library was screened with a probe amplified

CC using primers 30.2 and 43.3.RC(AA052476 and AA052477, respectively)

CC which were based on sequences of isolated NIF peptide fragments. Seven

CC of the 120 positive clones were isolated for sequence analysis. One

CC isolate, designated clone 1FL, encoded an 825 nucleotide open reading  
CC frame (AA052475). The other clones contained partial ORFs and encoded  
CC partial NIF polypeptides (see AAR52985-R32900) which are thought to  
CC represent six NIF isoforms that are significantly similar to, but  
CC not identical to, the prototypical NIF-1FL polypeptide (AAR42488).

SO Sequence 231 AA;

Query Match 29.9%; Score 298; DB 14; Length 231;  
Best Local Similarity 35.7%; Pred. No. 1.3e-22;

Matches 75; Conservative 20; Mismatches 57; Indels 58; Gaps 9;

OY 6 LCQOREK---LDDMRKEMTEELNGYRAAFARNY----- 36  
DB 16 ICSQNGTGMEFGFNDMSRLKFLKLEMHNGYRSLALGHISITEPEESYDDDDGYGEVLAP 75  
OY 37 KTSKMRMYDCTLEEKAYKSAKSCSEPSSE-----EENVDFSAATLNIPLA 86  
DB 76 SASKRRMYEYDCEAEKSAKSAKSCSDSSSPGEGYDENKYLENSNISERARLAI----- 131  
OY 87 GNSWSEIFEL---RGKYNNKNGKTSNIANWVDSHDKIGCAVYDCSGK-----SGKT-HYV 136  
DB 132 -LSWAKKAFDLNKTGEGVLYRSNLTISNFANLAMDREKFGCAVAKCPLEDTSATTHYV 190  
OY 137 COYGEPAK---DGKTIYEGAPCSRCSY 163  
DB 191 CHY-PKIEGEKEKQIYKVGTPCGDCSEY 219

RESULT 8

AAY23605  
ID AAY23605 standard; Protein: 267 AA.

AC AAY23605;

DT 03-SEP-1999 (first entry)

DE Canine hookworm neutrophil inhibitory factor AcaniF6 polypeptide.

KW Neutrophil inhibitory factor; NIF; mutant; shock; stroke;

KW allograft rejection; vasculitis; autoimmune diabetes; ARDS;

KW rheumatoid arthritis; inflammatory skin disease; myocardial infarction;

KW inflammatory bowel disease; adult respiratory distress syndrome;

KW ischemia-reperfusion injury; acute inflammation; bacterial infection;

KW vaccine; parasitic worm infection; antihelminic.

OS Ancylostoma caninum.

PN US5919900-A.

PD 06-JUL-1999.

PE 26-MAY-1995; 95US-0450497.

PR 23-DEC-1993; 93US-0173510.

PR 11-MAY-1992; 92US-0881721.

PR 24-DEC-1992; 92US-0996972.

PR 11-MAY-1993; 93US-0060433.

PR 10-NOV-1993; 93US-0151064.

PR 26-MAY-1995; 95US-0450497.

PA (CORV-) CORVAS INT INC.

PI Foster DL, Moyle M;

PI 1999-403975/34.

PI N-PSDB; AAX85542.

PT Mutant Neutrophil Inhibitory Factors useful for treating

PT inflammatory conditions and especially to prevent or decrease

PT inflammatory responses

PS Example 21; Fig 16a-V; 131pp; English.

XX The specification describes mutant Neutrophil Inhibitory Factors (NIFs),  
 CC where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197,  
 CC or 223 in the wild type sequence (see AAY23591) is replaced by a Gln  
 CC residue. NIFs may be useful for treating shock, stroke, acute and  
 CC chronic allograft rejection, vasculitis, autoimmune diabetes, rheumatoid  
 CC arthritis, inflammatory skin diseases, inflammatory bowel disease, adult  
 CC respiratory distress syndrome (ARDS), ischemia-reperfusion injury  
 CC following myocardial infarction, and acute inflammation caused by  
 CC bacterial infection such as sepsis or bacterial meningitis. NIFs or NIF  
 CC fragments may be used as vaccines against parasitic worm infection.  
 CC Anti-NIF antibodies may be useful for detecting infection of a mammalian  
 CC host by a parasitic worm, as antihelminthic agents, and in the detection  
 CC and isolation of NIF from tissue homogenates, cloned cells etc. NIFs may  
 CC be useful for the detection of NIF mimics or antagonists in other  
 CC compounds. Other NIF agonists and inhibitors may also be used as  
 CC antihelminthic agents. AAY23600-10 represent canine hookworm NIF proteins.  
 CC  
 SO Sequence 267 AA;  
 Query Match 29.7%; Score 296.5; DB 20; Length 267;  
 Best Local Similarity 34.3%; Pred. No. 2.3e-22;  
 Matches 72; Conservative 22; Mismatches 63; Indels 53; Gaps 7;  
 DB 6 LCOOREK---LDDMRKEMFTELHGGRFAAFANY-----KT 38  
 19 MCOQNETMPGFNDLRLQFLAMNGYRSKIALGHISTDESDYDYGFDPDPAPSA 78  
 QY 39 SKMRTMYDCTLEEKAYKSAEKCEE---PSSEBNVDYFSATLNT---PLEGNSMWS 92  
 DB 79 SKMRYLEYDCEAKRSATYSASDCSDSSPPEGYDENKTYFENSN-NISEALKAMISMAK 137  
 QY 93 EIFEL---RGKYNNKNGKTSNIANNVWDSDHDKGCAVYDC-----SGKT 133  
 DB 138 EAFNLNTEKGVLYQPNHDISFNFLANDVREKFGCAVYNCPLGIDADYDEETATYTI 197  
 QY 134 HVCYGYPEAKGDKTYEGAPCSRCSDY 163  
 DB 198 HVCYHPKINKTEGEPIYKVGTPCDDCSEY 227  
 RESULT 9  
 AAY23603  
 ID AAY23603 standard; Protein: 270 AA.  
 AC AAY23603;  
 XX  
 DT 03-SEP-1999 (first entry)  
 XX  
 DE Canine hookworm neutrophil inhibitory factor AcanIF3 polypeptide.  
 XX  
 KW Neutrophil inhibitory factor; NIF; mutant; shock; stroke;  
 KW allograft rejection; vasculitis; autoimmune diabetes; ARDS;  
 KW rheumatoid arthritis; inflammatory skin disease; myocardial infarction;  
 KW inflammatory bowel disease; adult respiratory distress syndrome;  
 KW ischemia-reperfusion injury; acute inflammation; bacterial infection;  
 KW vaccine; parasitic worm infection; antihelminthic.  
 XX  
 OS Ancylostoma caninum.  
 XX  
 PN US5919900-A.  
 XX  
 PD 06-JUL-1999.  
 XX  
 DE 26-MAY-1995; 9505-0450497.  
 XX  
 PE 23-DEC-1993; 9305-0173510.  
 PR 11-MAY-1992; 9205-0881721.  
 PR 24-DEC-1992; 9205-0996972.  
 PR 11-MAY-1993; 9305-0060433.  
 PR 10-NOV-1993; 9305-0151064.  
 PR 26-MAY-1995; 9505-0450497.  
 XX

PA (CORV-) CORVAS INT INC.  
 XX  
 XX Foster DL, Moyle M;  
 XX  
 XX WPI: 1999-403975/34.  
 DR N-PSDB; AAY85540.  
 XX  
 PT Mutant Neutrophil Inhibitory Factors useful for treating  
 PT inflammatory conditions and especially to prevent or decrease  
 PT inflammatory responses  
 PS  
 PS Example 21; Fig 16A-V; 131pp; English.  
 CC  
 CC The specification describes mutant Neutrophil Inhibitory Factors (NIFs),  
 CC where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197,  
 CC or 223 in the wild type sequence (see AAY23591) is replaced by a Gln  
 CC residue. NIFs may be useful for treating shock, stroke, acute and  
 CC chronic allograft rejection, vasculitis, autoimmune diabetes, rheumatoid  
 CC arthritis, inflammatory skin diseases, inflammatory bowel disease, adult  
 CC respiratory distress syndrome (ARDS), ischemia-reperfusion injury  
 CC following myocardial infarction, and acute inflammation caused by  
 CC bacterial infection such as sepsis or bacterial meningitis. NIFs or NIF  
 CC fragments may be used as vaccines against parasitic worm infection.  
 CC Anti-NIF antibodies may be useful for detecting infection of a mammalian  
 CC host by a parasitic worm, as antihelminthic agents, and in the detection  
 CC and isolation of NIF from tissue homogenates, cloned cells etc. NIFs may  
 CC be useful for the detection of NIF mimics or antagonists in other  
 CC compounds. Other NIF agonists and inhibitors may also be used as  
 CC antihelminthic agents. AAY23600-10 represent canine hookworm NIF proteins.  
 CC  
 SO Sequence 270 AA;  
 Query Match 29.7%; Score 296.5; DB 20; Length 270;  
 Best Local Similarity 34.3%; Pred. No. 2.3e-22;  
 Matches 72; Conservative 22; Mismatches 63; Indels 53; Gaps 7;  
 DB 6 LCOOREK---LDDMRKEMFTELHGGRFAAFANY-----KT 38  
 22 MCOQNETMPGFNDLRLQFLAMNGYRSKIALGHISTDESDYDYGFDPDPAPSA 81  
 QY 39 SKMRTMYDCTLEEKAYKSAEKCEE---PSSEBNVDYFSATLNT---PLEGNSMWS 92  
 DB 82 SKMRYLEYDCEAKRSATYSASDCSDSSPPEGYDENKTYFENSN-NISEALKAMISMAK 140  
 QY 93 EIFEL---RGKYNNKNGKTSNIANNVWDSDHDKGCAVYDC-----SGKT 133  
 DB 141 EAFNLNTEKGVLYQPNHDISFNFLANDVREKFGCAVYNCPLGIDADYDEETATYTI 200  
 QY 134 HVCYGYPEAKGDKTYEGAPCSRCSDY 163  
 DB 201 HVCYHPKINKTEGEPIYKVGTPCDDCSEY 230  
 RESULT 10  
 AAY23593  
 ID AAY23593 standard; Protein: 232 AA.  
 AC AAY23593;  
 XX  
 DT 03-SEP-1999 (first entry)  
 XX  
 DE Canine hookworm neutrophil inhibitory factor isoform clone 3P.  
 XX  
 KW Neutrophil inhibitory factor; NIF; mutant; shock; stroke;  
 KW allograft rejection; vasculitis; autoimmune diabetes; ARDS;  
 KW rheumatoid arthritis; inflammatory skin disease; myocardial infarction;  
 KW inflammatory bowel disease; adult respiratory distress syndrome;  
 KW ischemia-reperfusion injury; acute inflammation; bacterial infection;  
 KW vaccine; parasitic worm infection; antihelminthic.  
 XX  
 OS Ancylostoma caninum.  
 XX  
 PN US5919900-A.

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XX PD 06-JUL-1999.
XX PF
XX 26-MAY-1995; 950S-0450497.
XX
XX 23-DEC-1993; 930S-0173510.
XX 11-MAY-1992; 920S-0881721.
XX 24-DEC-1992; 920S-0996972.
XX 11-MAY-1993; 930S-0060433.
XX 10-NOV-1993; 930S-0151064.
XX 26-MAY-1995; 950S-0450497.
PA (CORV-) CORVAS INT INC.
PI
PI Foster DL, Moyle M;
XX WPI; 1999-403975/34.
XX
XX Mutant Neutrophil Inhibitory Factors useful for treating
XX PT inflammatory conditions and especially to prevent or decrease
XX PT inflammatory responses
XX PS
XX PS Example 10; Fig 9A-E; 131pp; English.
XX
XX The specification describes mutant Neutrophil Inhibitory Factors (NIFs),
XX CC where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197,
XX CC or 223 in the wild type sequence (see MA23591) is replaced by a Glu
XX CC residue. NIFs may be useful for treating shock, stroke, acute and
XX CC chronic allograft rejection, vasculitis, autoimmune diabetes, rheumatoid
XX CC arthritis, inflammatory skin diseases, inflammatory bowel disease, adult
XX CC respiratory distress syndrome (ARDS), ischemic reperfusion injury
XX CC following myocardial infarction, and acute inflammation caused by
XX CC bacterial infection such as sepsis or bacterial meningitis. NIFs or NIF
XX CC fragments may be used as vaccines against parasitic worm infection.
XX CC Anti-NIF antibodies may be useful for detecting infection of a mammalian
XX CC host by a parasitic worm, as antihelminthic agents, and in the detection
XX CC and isolation of NIF from tissue homogenates, cloned cells etc. NIFs may
XX CC be useful for the detection of NIF mimics or antagonists in other
XX CC compounds. Other NIF agonists and inhibitors may also be used as
XX CC antihelminthic agents. MA23592-98 represent isoform clones of canine
XX CC hookworm NIF.
XX
XX Sequence 232 AA;
SQ
Query Match 29.1%; Score 290.5; DB 20; Length 232;
Best Local Similarity 37.3%; Pred. No. 8e-22;
Matches 75; Conservative 23; Mismatches 60; Indels 43; Gaps 7.
OY 1 EGDYSLCORFKL---DDMRKEMTEHLNHYRAAFKRY-----K 37
DB 37 EHDPTCPQNGKKMKKGGPDALIKRLKLANHNRSLALGHVSTIEESDYIDLALAPR 96
OY 38 TSKMTNHYDCTLEBKNAISAKCESEESSE---ENV-----DVSATNTPLNG 87
DB 97 ASKNRYLKYDCEAKENKATSESAKCTQTASSKEKIDENLOYIEDPDINHAA-----LKA 151
OY 88 NNMSEFEFL-----RKNYNNKGTSTRIANNWDSHDKLGCAVVDSCSK-TRVVCYGP 142
DB 152 ISMTAEFNLNKTKGEGVYRSLTIDISNFPANLADTREKVCAGVAVCSFRTTHVCHYPRK 211
OY 143 AKGDGKITYEEGAPCSKSDY 163
DB 212 SRKKNPITYTGNRCGCSDY 232
RESULT 11
AAE20891
ID AAE20891 standard; Protein; 257 AA.
AC
AC AAE20891;
XX 01-JUL-2002 (first entry)
XX

```

DE	Ancylostoma caninum mature neutrophil inhibitory factor (NIF) 1 protein.
KW	Neutrophil inhibitory factor; NIF; therapy; inflammatory condition;
KM	abnormal neutrophil activation; shock; stroke; allograft rejection;
KV	vasculitis; autoimmune diabetes; rheumatoid arthritis; head trauma;
KW	inflammatory skin disease; inflammatory bowel disease; antibacterial;
KM	adult respiratory distress syndrome; ARDS; ischemia-reperfusion injury;
KM	bacterial infection; bacterial infection; sepsis; cerebroprotective;
KW	myocardial infarction; immunosuppressive; antiparasitic; antihelmintic;
KM	vaccine; antiinflammatory; vasotropic.
OS	Ancylostoma caninum.
PX	WO200216584-A2.
PN	
PD	28-FEB-2002.
PP	15-AUG-2001; 2001MO-US25733.
PR	23-AUG-2000; 2000US-0649442.
PR	28-FEB-2001; 2001US-0797410.
XX	(PE12 ) PFIZER PROD INC.
PA	(CORV-) CORVAS INT INC.
XX	
PI	Plushchell SB, Geldard RW, Ho L, Koehler MA, Okedadi CA, Plas SJ,
PI	Zhu MM, Hawrylyk SJ, Moyle M,
DR	WPI; 2002-292063/33.
PT	Preparing Neutrophil Inhibitory Factor for treating shock, by growing
PT	cell line expressing the factor in animal component-free medium such as
PT	Inoculum growth medium, production growth medium or nutrient feed
XX	
PS	Claim 42; Page 92-94; 10pp; English.
CC	The invention relates to a method for the preparation of neutrophil
CC	inhibitory factor (NIF) comprising growing a cell line expressing NIF
CC	in an animal component-free medium selected from inoculum growth medium,
CC	a production growth medium and a nutrient feed to give a production
CC	culture. The method is useful for preparation of NIF. Animal component-
CC	-free production growth medium is useful for preparation of recombinant
CC	proteins. NIF is useful for preventing or treating inflammatory
CC	conditions characterised by abnormal neutrophil activation, for
CC	shock, stroke, acute and chronic allograft rejection, vasculitis,
CC	autoimmune diabetes, rheumatoid arthritis, head trauma, inflammatory
CC	skin diseases, inflammatory bowel disease, adult respiratory distress
CC	syndrome (ARDS), ischemia-reperfusion injury following myocardial
CC	infarction, in which neutrophil infiltration and activation has been as
CC	implicated and acute inflammation caused by bacterial infection, such as
CC	sepsis or bacterial meningitis. NIF is also useful as diagnostic agents,
CC	to screen other compounds to detect NIF mimics or to detect NIF
CC	antagonists for their ability to affect NIF binding to the CD1b/CD18
CC	receptor, as a vaccine against parasitic worm infections in mammals, and
CC	for prophylaxis and therapy of parasitic infections. The present sequence
CC	is Ancylostoma caninum mature NIF1 protein.
XX	
SQ	Sequence 257 AA:
Query Match	29.1%; Score 290; DB 23; Length 257;
Best Local Similarity	34.3%; Pred. No. 1e-21;
Matches 69; Conservative 23; Mismatches 57; Indels 52; Gaps 7	
OY	14 DDMREMTLHNCRYRAAFARNY-----KTSKARTMYGCTL 50
DB	18 NSDIRGLPLAHNNYYSKALALGHISTIEBESDDDDGFLPDPAPASKMYLTLYDEA 77
OY	51 EKAYKSAKCSSE--PSSEENVDVFSATLNT---PLEANGSWWSIEFPL-----R 98
DB	78 EKATYSARNCSOSSSPGPGIDENKTTFEENS-NISEALAKAMISNAKEFNLFNTKEGE 136
OY	99 GAVYNKNSRTSINLAAMYWDSDHKLCACAYDC-----SKT-----HYVCQGP 142

Dd		137	GVALRSNHDISNFALMLAMDRERFGCAVYNNCLGEIDDETFNHDEGTATTTIHVCYPKI	196
Oy		143	AKGQKTIYEAGAPCSCSDY	163
		:   :	:   :   :   :	
Dd		197	NRTGGPIYKVGCTPCDDCSEX	217
 RESULT 12 AAAY23606 ID MAY23606 standard; Protein: 272 AA.				
XX	AC	AAAY23606;		
XX	DF	03-SEP-1999 (first entry)		
XX	DE	Canine hookworm neutrophil inhibitory factor AcanNf7 polypeptide.		
KM	RW	Neutrophil inhibitory factor: NIF; mutant; shock; stroke;		
KM	RW	allergic rejection; vasculitis; autoimmune diabetes; ARDS;		
KM	RW	rheumatoid arthritis; inflammatory skin disease; myocardial infarction;		
KM	RW	inflammatory bowel disease; adult respiratory distress syndrome;		
KM	RW	ischemia-reperfusion injury; acute inflammation; bacterial infection;		
KM	RW	vaccine; parasitic worm infection; antihelminic.		
XX	OS	Ancylostoma caninum.		
XX	PX	US5919900-A.		
XX	PX	06-JUL-1999.		
XX	PX	26-MAY-1995; 95US-0450497.		
XX	PR	23-DEC-1993; 93US-0173510.		
XX	PR	11-MAY-1992; 92US-0881721.		
XX	PR	24-DEC-1992; 92US-0996972.		
XX	PR	11-MAY-1993; 93US-0060433.		
XX	PR	10-NOV-1993; 93US-0151064.		
XX	PR	26-MAY-1995; 95US-0450497.		
PA	(CORV)	CORVAS INT INC.		
PI	Foster DL,	Moyle M;		
DR	WPI:	1999-403975/34.		
XX	N-PDB:	ANK85343.		
PT	Mutant Neutrophil Inhibitory Factors useful for treating			
FT	Inflammatory conditions and especially to prevent or decrease			
PT	Inflammatory responses			
XX	Example 21: F1g 16A-V; 131pp; English.			
PS	The specification describes mutant Neutrophil Inhibitory Factors (NIFs).			
XX	where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197,			
CC	or 223 in the wild type sequence (see AAAY23591) is replaced by a Gln			
CC	residue. NIFs may be useful for treating shock, stroke, acute and			
CC	chronic allograft rejection, vasculitis, autoimmune diabetes, rheumatoid			
CC	arthritis, inflammatory skin diseases, inflammatory bowel disease, adult			
CC	respiratory distress syndrome (ARDS), ischemia-reperfusion injury			
CC	following myocardial infarction, and acute inflammation caused by			
CC	bacterial infection such as sepsis or bacterial meningitis. NIFs or NIF			
CC	fragments may be used as vaccines against parasitic worm infection.			
CC	Anti-NIF antibodies may be useful for detecting infection of a mammalian			
CC	host by a parasitic worm, as antihelminic agents, and in the detection			
CC	and isolation of NIF from tissue homogenates, cloned cells etc. NIFs may			
CC	be useful for the detection of NIF mimics or antagonists in other			
CC	compounds. Other NIF agonists and inhibitors may also be used as			
CC	antihelminic agents. AAAY23600-10 represent canine hookworm NIF proteins.			
XX	Sequence	272 AA:		
Query Match	29.1%; Score 290; DB 20; Length 272;			
Best Local Similarity	34.3%; Pfd. No. 1,Je-21;			

```

Matches      69;  Conservative      23;  Mismatches      57;  Indels      52;  Gaps      7
OY          14 DDDMRMFEFLHNGYRAAFARNY-----KTSKMTWVDCITL 50
Db          33 NDSIRLQFLAHNGYRSKTLALGHISTEESDDDDDFGLPDPAPRAASKMYLEYDCA 92
OY          51 EEKAYSAKSGSEE---PSEEEVNDVFAAATLT---PLEAGSNMWSIEPFL-----R 98
Db          93 EKAAYSAKSNCSDDSSPFCYDENEKTYIFENSN-NISEAALAKMIMSNAKAFPLNKEBS 151
OY          99 GKTYNNKGTNTNANWMSHDKGCAVYDC-----SKT-----HYVCGPGE 142
Db          152 GVLRSNHDISFNFLNLMARKRECECAVNCPLGEIDETHDDEYATTHVCHTPIK 211
OY          143 AKGDGKTYIEGAPCSRSDY 163
Db          212 NKTGGPIIKVGTPTCDCCSEY 232

RESULT 13
AAR42488
ID AAR42488 standard; Protein; 274 AA.
XX
XX AAR42488;
XX
XX 02-JUN-1994 (first entry)
XX
XX Canine hookworm Neutrophil Inhibitory Factor 1FL.
XX
XX Neutrophil Inhibitory factor; NIF, glycoprotein; endoparasite;
XX nematode; parasitic worm; canine hookworm, peritoneal inflammation.
XX
XX Ancylostoma caninum.
XX
XX PN W09323063-A.
XX
XX 25-NOV-1993.
XX
XX 11-MAY-1993; 93MO-US04502.
XX
XX 11-MAY-1992; 92US-0881271.
XX
XX 24-DEC-1992; 92US-0996972.
XX
XX (CONV-) CORVAS INT INC.
XX
XX Foster DL; Moyle M, Vlasuk GP;
XX
XX WPI; 1993-386208/48.
XX
XX N-PSDB; AA052475.
XX
XX
XX New neutrophil inhibitory factor from parasitic worms - for
XX preventing and treating inflammation, also derived nucleic acid,
XX vectors, transformed hosts and antibodies
XX
XX Claim 23; Fig 8; 114pp; English.
XX
XX A canine hookworm cDNA library was screened with a probe amplified
XX using primers 30.2 and 43.3 (AA052476 and AA052477, respectively) which
XX were based on sequences of isolated NIF peptide fragments. Seven of
XX the 120 positive clones were isolated for sequence analysis. One
XX isolate, designated clone 1FL, encoded an 825 nucleotide open reading
XX frame (AA052475). The other clones contained partial ORFs and encoded
XX partial NIF polypeptides (see AA852985-R52990) which are thought to
XX represent six NIF isoforms that are significantly similar to, but
XX not identical to, the prototypical NIF-1FL polypeptide (AAR42488).
XX
XX Sequence      274 AA.

Query Match      29 18; Score 290; DB 14; Length 274;
Best Local Similarity 34.38; Pred. No. 1.1e-21;
Matches 69; Conservative 23; Mismatches 57; Indels 52; Gaps 7;
OY          14 DDDMRMFEFLHNGYRAAFARNY-----KTSKMTWVDCITL 50

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DB      35 NDSIRLOFLAMHNGYRSKLAIGHISTESESDDDDGFLPDPAPRASKMYLEIDCEA 94
OY      51 EERAYSAKNCSE--PSEENVDFSAATLNI---PLEANGSMSEIFEL-----R 98
DB      95 EKSAVMSARNCSDSSPEEGYDENKIFENS-NISEAALAMISMAREFNLNKTKEG 153
OY      99 GKYVNRNGKTSNINAMWDSHDKLCCAVYDC-----SGKT-----HYVCOGPE 142
DB      154 GVLIRSNHDSINFNALMDAREFGCAVNCPLGEIDETNHDETYATIHVCHYPKI 213
OY      143 AKDGKTYIEGAPCSRCSY 163
DB      214 NRTGDPITYKGTPCDCSER 234

RESULT 14
AA23600
ID      AA23600 standard; Protein: 274 AA.
AC      XX
XX      AA23600;
DT      03-SEP-1999 (first entry)
DE      Canine hookworm neutrophil inhibitory factor NIF-1FL polypeptide.
XX      XX
XX      Neutrophil inhibitory factor; NIF; mutant; shock; stroke;
XX      Allergic rejection; vasculitis; autoimmune diabetes; ARDS;
XX      Rheumatoid arthritis; inflammatory skin disease; myocardial infarction;
XX      Inflammatory bowel disease; adult respiratory distress syndrome;
XX      Ischemia-reperfusion injury; acute inflammation; bacterial infection;
XX      vaccine; parasitic worm infection; antihelminic.
XX      Ancylostoma caninum.
OS      US5919900-A.
PN      06-JUL-1999.
PD      26-MAY-1995; 95US-0450497.
XX      XX
XX      23-DEC-1993; 93US-0173510.
XX      11-MAY-1992; 92US-0881721.
XX      24-DEC-1992; 92US-0996972.
XX      11-MAY-1993; 93US-0060433.
XX      10-NOV-1993; 93US-0151064.
XX      26-MAY-1995; 95US-0450497.
XX      XX
XX      (CORV-) CORVAS INT INC.
XX      PA
XX      Foster DL, Moyle M;
XX      WPI; 1999-403975/34.
XX      DR
XX      N-PSDB; AAX85537.
XX      XX
XX      Mutant Neutrophil Inhibitory Factors useful for treating
XX      inflammatory conditions and especially to prevent or decrease
XX      inflammatory responses
XX      XX
XX      Example 21; Fig 16A-V; 131pp; English.
XX      XX
XX      The specification describes mutant Neutrophil Inhibitory Factors (NIFs),
XX      where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197,
XX      or 224 in the wild type sequence (see AA23591) is replaced by a Glu
XX      residue. NIFs may be useful for treating shock, stroke, acute and
XX      chronic allergic rejection, vasculitis, autoimmune diabetes, rheumatoid
XX      arthritis, inflammatory skin diseases, inflammatory bowel disease, adult
XX      respiratory distress syndrome (ARDS), ischemia-reperfusion injury
XX      following myocardial infarction, and acute inflammation caused by
XX      bacterial infection such as sepsis or bacterial meningitis. NIFs or NIF
XX      fragments may be used as vaccines against parasitic worm infection.
XX      Anti-NIF antibodies may be useful for detecting infection of a mammalian
XX      host by a parasitic worm, as antihelminic agents, and in the detection

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CC      and isolation of NIF from tissue homogenates, cloned cells etc. NIFs may
CC      be useful for the detection of NIF mimics or antagonists in other
CC      compounds. Other NIF agonists and inhibitors may also be used as
CC      antihelminic agents. AA23600-10 represent canine hookworm NIF proteins.
XX      XX
XX      Sequence 274 AA;
XX      50
XX      Query Match 29.1%; Score 290; DB 20; Length 274;
XX      Best Local Similarity 34.3%; Pred. No. 1,1e-21;
XX      Matches 69; Conservative 23; Mismatches 57; Indels 52; Gaps 7;
OY      14 DDDMRNETELHNGYNAFAARNY-----KTSKRTVYDCTL 50
DB      35 NDSIRLOFLAMHNGYRSKLAIGHISTESESDDDDGFLPDPAPRASKMYLEIDCEA 94
OY      51 EERAYSAKNCSE--PSEENVDFSAATLNI---PLEANGSMSEIFEL-----R 98
DB      95 EKSAVMSARNCSDSSPEEGYDENKIFENS-NISEAALAMISMAREFNLNKTKEG 153
OY      99 GKYVNRNGKTSNINAMWDSHDKLCCAVYDC-----SGKT-----HYVCOGPE 142
DB      154 GVLIRSNHDSINFNALMDAREFGCAVNCPLGEIDETNHDETYATIHVCHYPKI 213
OY      143 AKDGKTYIEGAPCSRCSY 163
DB      214 NRTGDPITYKGTPCDCSER 234

RESULT 15
AA23601
ID      AA23601 standard; Protein: 274 AA.
AC      XX
XX      AA23601;
DT      03-SEP-1999 (first entry)
DE      Canine hookworm neutrophil inhibitory factor PCR-NIF7 polypeptide.
XX      XX
XX      Neutrophil inhibitory factor; NIF; mutant; shock; stroke;
XX      Allergic rejection; vasculitis; autoimmune diabetes; ARDS;
XX      Rheumatoid arthritis; inflammatory skin disease; myocardial infarction;
XX      Inflammatory bowel disease; adult respiratory distress syndrome;
XX      Ischemia-reperfusion injury; acute inflammation; bacterial infection;
XX      vaccine; parasitic worm infection; antihelminic.
XX      Ancylostoma caninum.
OS      US5919900-A.
PN      06-JUL-1999.
PD      26-MAY-1995; 95US-0450497.
XX      XX
XX      23-DEC-1993; 93US-0173510.
XX      11-MAY-1992; 92US-0881721.
XX      24-DEC-1992; 92US-0996972.
XX      11-MAY-1993; 93US-0060433.
XX      10-NOV-1993; 93US-0151064.
XX      26-MAY-1995; 95US-0450497.
XX      XX
XX      (CORV-) CORVAS INT INC.
XX      PA
XX      Foster DL, Moyle M;
XX      WPI; 1999-403975/34.
XX      DR
XX      N-PSDB; AAX85538.
XX      XX
XX      Mutant Neutrophil Inhibitory Factors useful for treating
XX      inflammatory conditions and especially to prevent or decrease
XX      inflammatory responses
XX      XX
XX      Example 21; Fig 16A-V; 131pp; English.
XX      XX

```

The specification describes mutant Neutrophil Inhibitory Factors (NIFs), where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197, or 223 in the wild type sequence (see AAY23591) is replaced by a Glu residue. NIFs may be useful for treating shock, stroke, acute and chronic allograft rejection, vasculitis, autoimmune diabetes, rheumatoid arthritis, inflammatory skin diseases, inflammatory bowel disease, adult respiratory distress syndrome (ARDS), ischemia-reperfusion injury, following myocardial infarction, and acute inflammation caused by bacterial infection such as sepsis or bacterial meningitis. NIFs or NIF fragments may be used as vaccines against parasitic worm infection. Anti-NIF antibodies may be useful for detecting infection of a mammalian host by a parasitic worm, as antihelminthic agents, and in the detection and isolation of NIF from tissue homogenates, cloned cells etc. NIFs may be useful for the detection of NIF mimics or antagonists in other compounds. Other NIF agonists and inhibitors may also be used as antihelminthic agents. AAY23591-10 represent canine hookworm NIF proteins.

Sequence 274 AA:

Query Match 29.1%; Score 290; DB 20; Length 274;  
Best Local Similarity 33.8%; Pred. No. 1.1e-21;  
Matches 72; Conservative 25; Mismatches 60; Indels 56; Gaps 9;

6 LCOQR---EKIDDKREKTELNGYRAFAFANY-----KT 38  
23 MCOQNGTEMPDNDSDIRLDFLMANGYRSKIALGHISTEESDDDDFGFLPDFAFRA 82  
39 SKMTMYDCTLEKAYKSAKCSSE---PSESEENVYFSAATINI---PLEAGNSMWS 92  
83 SMRTLEYDEAKSAVMSARNCSDSSPPGEGYENKTYFENSN-NISEALAKAMISMAK 141

93 ETEFL---RGK---VYNKNGKTSNIANNVMDSHDKLGCAYVDC-----SGRT-- 133  
142 EAFNINIKTEGEVEYLRSHNDISNFANLAMAREKFCAYVNCPLGEIDETIHDEGTVA 201  
202 TTIHVCHYPRINKTEGEPIYKVGTPDCDCEY 234

134 ---HYVCOYGEAKGCKTIYEGAPCSRCSY 163  
202 TTIHVCHYPRINKTEGEPIYKVGTPDCDCEY 234

RESULT 16  
ID AAY23592 standard; Protein; 274 AA.

AC AAY23592;  
DT 03-SEP-1999 (first entry)

XX Canine hookworm neutrophil inhibitory factor isoform clone 1FL.  
DE Neutrophil inhibitory factor; NIF; mutant; shock; stroke;  
KM allograft rejection; vasculitis; autoimmune diabetes; ARDS;  
KM rheumatoid arthritis; inflammatory skin disease; myocardial infarction;  
KM inflammatory bowel disease; adult respiratory distress syndrome;  
KM ischemia-reperfusion injury; acute inflammation; bacterial infection;  
KM vaccine; parasitic worm infection; antihelminthic.

XX Ancylostoma caninum.  
OS  
PN US5919900-A.  
XX  
PD 06-JUL-1999.  
XX  
PF 26-MAY-1995; 9505-0450497.  
XX  
PR 23-DEC-1993; 9305-0173510.  
PR 11-MAY-1992; 9205-0881721.  
PR 24-DEC-1992; 9205-0996972.  
PR 11-MAY-1993; 9305-0060433.  
PR 10-NOV-1993; 9305-0151064.  
PR 26-MAY-1995; 9505-0450497.  
XX  
PA (CORV-) CORVAS INT. INC.

XX Poster DL. Moyle M.  
PI  
XX WPI: 1999-403975/34.  
DR  
XX  
PT Mutant Neutrophil Inhibitory Factors useful for treating  
PT inflammatory conditions and especially to prevent or decrease  
PT inflammatory responses

XX Example 10; Fig 9A-E; 131pp; English.

The specification describes mutant Neutrophil Inhibitory Factors (NIFs), where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197, or 223 in the wild type sequence (see AAY23591) is replaced by a Glu residue. NIFs may be useful for treating shock, stroke, acute and chronic allograft rejection, vasculitis, autoimmune diabetes, rheumatoid arthritis, inflammatory skin diseases, inflammatory bowel disease, adult respiratory distress syndrome (ARDS), ischemia-reperfusion injury, following myocardial infarction, and acute inflammation caused by bacterial infection such as sepsis or bacterial meningitis. NIFs or NIF fragments may be used as vaccines against parasitic worm infection. Anti-NIF antibodies may be useful for detecting infection of a mammalian host by a parasitic worm, as antihelminthic agents, and in the detection and isolation of NIF from tissue homogenates, cloned cells etc. NIFs may be useful for the detection of NIF mimics or antagonists in other compounds. Other NIF agonists and inhibitors may also be used as antihelminthic agents. AAY23592-98 represent isoform clones of canine hookworm NIF.

Sequence 274 AA:

Query Match 29.1%; Score 290; DB 20; Length 274;  
Best Local Similarity 34.3%; Pred. No. 1.1e-21;  
Matches 69; Conservative 23; Mismatches 57; Indels 52; Gaps 7;

14 DDDMRKMFTELNGYRAFAFANY-----KTSKMTNYDCTL 50  
35 NDSIRLQFLAMNGYRSKIALGHISTEESDDDDFGFLPDFAFRAKMYLEYDCEA 94

51 EKAYKSAKCSSE---PSESEENVYFSAATINI---PLEAGNSMWSIFEFL-----R 98  
95 EKSAVMSARNCSDSSPPGEGYENKTYFENSN-NISEALAKAMISMAKFAFLNKTREGE 153

99 GKYNNKNGKTSNIANNVMDSHDKLGCAYVDC-----SGKT-----HYVCOYGE 142  
154 GVLIRSHNDISNFANLAMAREKFCAYVNCPLGEIDETIHDEGTVAATTIHYVCHYKFI 213

143 AKGDGKTIYEGAPCSRCSY 163  
214 NKTGEPITIKVGTPDCDCEY 234

RESULT 17  
ID AAY23591 standard; Protein; 274 AA.

AC AAY23591;  
DT 03-SEP-1999 (first entry)

XX Canine hookworm neutrophil inhibitory factor clone 1FL.  
DE Neutrophil inhibitory factor; NIF; mutant; shock; stroke;  
KM allograft rejection; vasculitis; autoimmune diabetes; ARDS;  
KM rheumatoid arthritis; inflammatory skin disease; myocardial infarction;  
KM inflammatory bowel disease; adult respiratory distress syndrome;  
KM ischemia-reperfusion injury; acute inflammation; bacterial infection;  
KM vaccine; parasitic worm infection; antihelminthic.

XX Ancylostoma caninum.  
OS  
PN US5919900-A.

PD 06-JUL-1999.  
 XX 26-MAY-1995; 95US-0450497.  
 XX 23-DEC-1993; 93US-0173510.  
 PR 11-MAY-1992; 92US-0881721.  
 PR 24-DEC-1992; 92US-0996972.  
 PR 11-MAY-1993; 93US-0060433.  
 PR 10-NOV-1993; 93US-0151064.  
 PR 26-MAY-1995; 95US-0450497.  
 XX (CORV-) CORVAS INT INC.  
 XX Foster DL, Moyle M;  
 XX WPI: 1999-403975/34.  
 DR N-PSDB; AAX85535.  
 XX  
 XX Mutant Neutrophil Inhibitory Factors useful for treating  
 PT inflammatory conditions and especially to prevent or decrease  
 PT inflammatory responses  
 PS Claim 1: Fig 8A-E; 131pp; English.  
 XX  
 XX The specification describes mutant Neutrophil Inhibitory Factors (NIFs),  
 CC where at least 1 of the Asp residues at positions 18, 87, 110, 130, 150,  
 CC or 223 in the wild type sequence (see AAY3591) is replaced by a Gln  
 CC residue. NIFs may be useful for treating shock, stroke, acute and  
 CC chronic allograft rejection, vasculitis, autoimmune diabetes, rheumatoid  
 CC arthritis, inflammatory skin diseases, inflammatory bowel disease, adult  
 CC respiratory distress syndrome (ARDS), ischemia-reperfusion injury  
 CC following myocardial infarction, and acute inflammation caused by NIF  
 CC bacterial infection such as sepsis or bacterial meningitis. NIFs or NIF  
 CC fragments may be used as vaccines against parasitic infection of a mammalian  
 CC host by a parasitic worm, as anti-infective agents, and in the detection  
 CC and isolation of NIF from tissue homogenates of cloned cells etc. NIFs may  
 CC be useful for the detection of NIFs in biological fluids or in other  
 CC compounds. Other NIF agonists and inhibitors may also be used as  
 CC anti-infective agents. The present sequence represents a canine hookworm  
 CC NIF.  
 XX  
 XX Sequence 274 AA;  
 S0  
 Query Match 29.1%; Score 290; DB 20; Length 274;  
 Best Local Similarity 34.3%; Pred. No. 1.1e-21;  
 Matches 69; Conservative 23; Mismatches 57; Indels 52; Gaps 7;  
 QY 14 DDDMEKTEFLHNGYRAAFARNY-----KTSKMTWVYDCTL 50  
 DB 35 NDSILQFLAMHNGYRSKALGHISTEESDDDDDFGLPDPFAPRAKMKRYLEYDCEA 94  
 QY 51 EKKAVSAEKSESE--PSSEENVDFSAATLNI--PLEAGNSWMSSEIFEL-----R 98  
 DB 95 EKSAYMSARNCSDSSSPPEGYDENKRYIFENSN-NISEALAKAMISWAKENAFMLNKEGE 153  
 QY 99 GKRYKNGKGTNSINAMWMDSHDKLGAAYVDC-----SGKT-----HVVCQYGP 142  
 DB 154 GYLRYRNDHDSINFNALMDAREKFGCAVVCPLGEIDETNHDGETYATVTHVCHYPKI 213  
 QY 143 AKGDGTYEKGAPCSCSDY 163  
 DB 214 NKEGQPIYKVGTPDDCSEY 234  
 RESULT 18  
 AAU97699  
 ID AAU97699 standard; Protein: 274 AA.  
 AC AAU97699;  
 XX  
 XX 13-AUG-2002 (first entry)  
 DT  
 XX

DE Canine hookworm Neutrophil Inhibitory Factor (NIF) protein sequence.  
 XX  
 XX Canine hookworm; dog hookworm; neutrophil inhibitory factor; NIF;  
 KW pathophysiological condition; neuroprotective; thrombolytic; stroke;  
 KW fibrinolytic; ischemic damage; reperfusion injury; head injury;  
 KW post-ischemic reperfusion injury; post-ischemic cerebral inflammation;  
 KW reperfusion-reperfusion injury; myocardial infarction; anti-inflammatory;  
 KW cardiac; synergist.  
 XX Ancylostoma caninum.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH Peptide 1-17  
 FT /label= Signal\_peptide  
 FT Protein 18-274  
 FT /label= Mature\_canine\_hookworm\_NIF\_protein  
 FT /note= "Specifically claimed in claim 2."  
 XX  
 XX WO200232446-A2.  
 XX  
 XX 25-APR-2002.  
 XX  
 XX 15-OCT-2001; 2001MO-IB01936.  
 XX  
 XX 17-OCT-2000; 2000GB-0025473.  
 XX  
 XX (PRIZ ) PRIZER LTD.  
 XX (PRIZ ) PRIZER INC.  
 XX  
 XX Bresley CJ, Butler P, Chaiwala SB, Chopp M, Krams M, Looby M;  
 PI Macintyre F, McElroy AB, McHarg AD;  
 DR WPI: 2002-452373/48.  
 XX N-PSDB; ABR52544.  
 XX  
 XX Use of a combination of at least one Neutrophil Inhibitory Factor and  
 PT at least one other neuroprotective or thrombolytic/fibrinolytic agent  
 PT for treating e.g. stroke, traumatic head injury or post-ischemic  
 PT cerebral inflammation  
 PS Claim 2; Fig 2; 110pp; English.  
 XX  
 XX The present invention relates to a new method for treating  
 CC pathophysiological conditions involving neutrophils. The method of the  
 CC invention involves administering to a subject, simultaneously/separately/  
 CC sequentially Neutrophil Inhibitory Factor (NIF) and another  
 CC neuroprotective or thrombolytic/fibrinolytic agent or a its  
 CC pharmaceutical salt, where the agents are effective in amounts that render  
 CC the combination of the 2 or more agents effective in treating  
 CC pathophysiological conditions involving neutrophils. The combination of  
 CC at least one Neutrophil Inhibitory Factor (NIF) and at least one other  
 CC neuroprotective or thrombolytic/fibrinolytic agent for the treatment of  
 CC pathophysiological conditions involving neutrophils is ischemic damage  
 CC and/or reperfusion injury e.g. stroke, traumatic head injury,  
 CC post-ischemic reperfusion injury, post-ischemic cerebral inflammation  
 CC or reperfusion-reperfusion injury following myocardial infarction.  
 CC The present amino acid sequence represents the canine (dog) hookworm  
 CC Neutrophil Inhibitory Factor (NIF) protein of the invention.  
 XX  
 XX Sequence 274 AA;  
 S0  
 Query Match 29.1%; Score 290; DB 23; Length 274;  
 Best Local Similarity 34.3%; Pred. No. 1.1e-21;  
 Matches 69; Conservative 23; Mismatches 57; Indels 52; Gaps 7;  
 QY 14 DDDMEKTEFLHNGYRAAFARNY-----KTSKMTWVYDCTL 50  
 DB 35 NDSILQFLAMHNGYRSKALGHISTEESDDDDDFGLPDPFAPRAKMKRYLEYDCEA 94  
 QY 51 EKKAVSAEKSESE--PSSEENVDFSAATLNI--PLEAGNSWMSSEIFEL-----R 98  
 DB 154 GYLRYRNDHDSINFNALMDAREKFGCAVVCPLGEIDETNHDGETYATVTHVCHYPKI 213  
 QY 143 AKGDGTYEKGAPCSCSDY 163  
 DB 214 NKEGQPIYKVGTPDDCSEY 234





KM	Rheumatoid arthritis; inflammatory skin disease; myocardial infection;
KM	Inflammatory bowel disease; adult respiratory distress syndrome;
KM	Ischemia-reperfusion injury; acute inflammation; bacterial infection;
KM	vaccine; parasitic worm infection; antihelminthic.
OS	Synthetic.
OS	Ancylostoma caninum.
XX	
PN	US9519900-A.
PD	06-JUL-1999.
XX	
PF	26-MAY-1995; 9505-0450497.
XX	
PR	23-DEC-1993; 9305-0173510.
PR	11-MAY-1992; 9205-0881721.
PR	24-DEC-1992; 9205-0996972.
PR	11-MAY-1993; 9305-0060433.
PR	10-NOV-1993; 9305-0151064.
PR	26-MAY-1995; 9505-0450497.
PA	(CORV-) CORVAS INT INC.
PI	Foster DL, Moyle M;
DR	WPI: 1999-403975/34.
NR	N-PDB: AAX85536.
XX	
PT	Mutant Neutrophil Inhibitory Factors useful for treating
PT	inflammatory conditions and especially to prevent or decrease
PT	inflammatory responses
XX	
PS	Example 20; Fig 15A-D; 131pp; English.
CC	The specification describes mutant Neutrophil Inhibitory Factors (NIFs),
CC	where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197,
CC	or 223 in the wild type sequence (see AY23591) is replaced by a Gln
CC	residue. NIFs may be useful for treating shock, stroke, acute and
CC	chronic allograft rejection, vasculitis, autoimmune bowel disease, rheumatoid
CC	arthritis, inflammatory skin diseases, inflammatory blood disease, adult
CC	respiratory distress syndrome (ARDS), ischemia-reperfusion injury
CC	following myocardial infarction, and acute inflammation caused by
CC	bacterial infection such as sepsis or bacterial meningitis. NIFs or NIF
CC	fragments may be used as vaccines against parasitic worm infection.
CC	Anti-NIF antibodies may be useful for detecting infection of a mammalian
CC	host by a parasitic worm, as anthelmintic agents, and in the detection
CC	and isolation of NIF from tissue homogenates, cloned cells etc. NIFs may
CC	be useful for the detection of NIF mimics or antagonists in other
CC	compounds. Other NIF agonists and inhibitors may also be used as
CC	anthelmintic agents. The present sequence is encoded by a two-distron
CC	Met-NIF expression cassette of Pma5-NI1/3.
XX	
XX	
XX	
Sequence	289 AA:
Q0	
Query Match	29.1%; Score 290; DB 20; Length 289;
Best Local Similarity	34.3%, Pred NO.1, 2e-22;
Matches	69; Conservative 23; Mismatches 57; Indels 52; Gaps 7
Oy	14 DDDREHFEELNGYBAFAAN-----KTSKRRTMYDYCTL 50
Dd	50 NDSIRDFPLAHMNGRKSLALGHITSESSDDEDDFGFLDPFAPRSKKRRLLEYDECA 105
Oy	51 EERYSASAKGEF---PSEEENDVFSAATLNT---PLEAGNSMWSEIFEL-----R 98
Dd	110 EKSYIVSANGCDSSPEEGIDENKTITENS-NISBALKAMISWAKEAFNLNKTKIGE 166
Oy	99 GKTYNNKGTSTIANMYWDSDHRGLCAVVC-----SGKT-----HYVCQYPE 142
Dd	169 GVLRSRNHDSISFNALMDAREFCGAVVNCPLGEIDETNHGDGETYAATTIHVCYPKI 228
Oy	143 AKDGKTYIEGACSCSCSDY 163
Dd	229 NKTEGGPIYKVTCPDCDCSEY 249

YY	35	NDSIRJFETFLMANGYKSKATLGHSTIEESBDDDDFCGLPDEFPARSKRRVLEYDCA	94
XX	34	DODMEKEFTLEHNGYBAFAFRNY-----KTSKKRMIVYDCIL	50
XZ	14	-----	7
XX	06	MATCHES 69; CONSERVATIVE 22; MISMATCHES 58; INDELS 52; GAPS 7.	
XX	DB	28.88; SCORE 287; DB 20; LENGTH 274;	
XX	DB	PRED. NO. 2.3e-21;	
XX	DB	Sequence 274 AA;	
XX	DB	Neutrophil Inhibitory factor; NIF; mutant; shock; stroke;	
XX	DB	Allergic rejection; vasculitis; autoimmune diabetes; ARDS;	
XX	DB	Rheumatoid arthritis; inflammatory skin disease; myocardial infarction;	
XX	DB	Inflammatory bowel disease; adult respiratory distress syndrome;	
XX	DB	Ischemia-reperfusion injury; acute inflammation; bacterial infection;	
XX	DB	Vaccine; parasitic worm infection; antihelminic.	
XX	DB	Ancylostoma caninum.	
XX	DB	US5919900-A.	
XX	DB	06-JUL-1999.	
XX	DB	26-MAY-1995; 95US-0450497.	
XX	DB	23-DEC-1993; 93US-0173510.	
XX	DB	PR 11-MAY-1992; 92US-0881721.	
XX	DB	PR 24-DEC-1992; 92US-0996972.	
XX	DB	PR 11-MAY-1993; 93US-0060433.	
XX	DB	PR 10-NOV-1993; 93US-0151064.	
XX	DB	PR 26-MAY-1995; 95US-0450497.	
XX	DB	(CORV-) CORVAS INT INC.	
XX	DB	Foster DL, Moyle M;	
XX	DB	WPI. 1999-403975/34.	
XX	DB	N-PSDB; AAX83544.	
XX	DB	Mutant Neutrophil Inhibitory Factors useful for treating	
XX	DB	Inflammatory conditions and especially to prevent or decrease	
XX	DB	Inflammatory responses	
XX	DB	Example 21; Fig 16A-V; 13pp; English.	
XX	DB	The specification describes mutant Neutrophil Inhibitory Factors (NIFs),	
XX	DB	where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197,	
XX	DB	or 223 in the wild type sequence (see AY23591) is replaced by a Glu	
XX	DB	residue. NIFs may be useful for treating shock, stroke, acute and	
XX	DB	chronic allograft rejection, vasculitis, autoimmune diabetes, rheumatoid	
XX	DB	arthritis, inflammatory skin diseases, inflammatory bowel disease, adult	
XX	DB	respiratory distress syndrome (ARDS), ischemia-reperfusion injury	
XX	DB	following myocardial infarction, and acute inflammation caused by	
XX	DB	bacterial infection such as sepsis or bacterial meningitis. NIFs or NIF	
XX	DB	fragments may be used as vaccines against parasitic worm infection.	
XX	DB	Anti-NIF antibodies may be useful for detecting infection of a mammalian	
XX	DB	host by a parasitic worm, as antihelminthic agents, and in the detection	
XX	DB	and isolation of NIF from tissue homogenates, cloned cells etc. NIFs may	
XX	DB	be useful for the detection of NIF mutants or antagonists in other	
XX	DB	compounds. Other NIF agonists and inhibitors may also be used as	
XX	DB	antihelminthic agents. AY23500-10 represent canine hookworm NIF proteins.	

```

Oy 51 EEKAKRSKSCSE--PSEEBNDVDSATLTNI--PLEAGNSWMSIFEL-----R 98
   1 : | | | | | : | : | : | : | : | : | : | : | : | : | : |
Db 95 EKSAYMSARNCSDDSSPECGEDENNYTFENSN-NISDALKAMISWAKFAFLNKTEGE 153
   1 : | | | | | : | : | : | : | : | : | : | : | : | : | : |
Oy 99 GKYYKRNKNTSTNINWMSHKLGCAYVDC-----SGKT-----HYVCQPE 142
   1 : | | | | | : | : | : | : | : | : | : | : | : | : | : |
Db 154 GVLVNSHNDISNFANLAMAOREKFCAYVNCPLGEIDETIHGEIYATTHVYCHPKI 213
   1 : | | | | | : | : | : | : | : | : | : | : | : | : | : |
Oy 143 AKGDGKTYEGCAPSCNSQSY 163
   1 : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 214 NKTSEQPIYKVGPCDDCSEX 234
   1 : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 22
AAR52985
ID AAR52985 standard; Protein; 234 AA.
XX
XX AAR52985:
XX
XX 02-JUN-1994 (first entry)
XX
XX Canine hookworm Neutrophil Inhibitory factor isoform 3p.
Db
XX neutrophil inhibitory factor; NIF; glycoprotein; endoparasitic;
XX nematode; parasitic worm; canine hookworm; peritoneal inflammation.
XX
XX Ancylostoma caninum.
XX
XX MO9323063-A.
XX
XX 25-NOV-1993.
XX
XX 11-MAY-1993; 93MO-USO4502.
XX
XX 11-MAY-1992; 92US-0881721.
XX
XX 24-DEC-1992; 92US-0996972.
XX
XX (CORV-) CORVAS INT INC.
XX
XX Foster DL, Moyle M, Vlaeuk GP;
XX
XX WPI; 1993-386208/48.
XX
XX New neutrophil inhibitory factor from parasitic worms - for
XX preventing and treating inflammation, also derived nucleic acid,
XX vectors, transformed hosts and antibodies
XX
XX Example 10; Fig 9; 114pp; English.
XX
XX
XX A canine hookworm cDNA library was screened with a probe amplified
XX using primers 30.2 and 43.3.RC(AAG52476 and AAG52477, respectively)
XX CC which were based on sequences of isolated NIF peptide fragments. Seven
XX CC of the 120 positive clones were isolated for sequence analysis. One
XX isolate, designated clone 1FL, encoded an 825 nucleotide open reading
XX CC frame (AAG52475). The other clones contained partial ORFs and encoded
XX CC partial NIF polypeptides (see AAR52985-R52890) which are thought to
XX represent six NIF isoforms that are significantly similar to, but
XX not identical to, the prototypical NIF-1FL polypeptide (AAR52488).
XX
XX
XX Sequence 234 AA:
XX
Oy Best Match 28 73; Score 286.5; DB 14; Length 234;
Db Query Similarity 36.93; Pred. No. 2.1e-21;
Matches 75; Conservative 22; Mismatches 61; Indels 45; Gaps 7
Oy 1 EGDYSLCQQRKL-----DDMKRETFELANGRYAARFRRNT----- 36
Db 37 EHDPLCPGNSKMEKGGDDAIRLKEFLAMHNSLALGHVSTIERSEDDYLDYDLIYAP 96
   1 : | | | | | : | : | : | : | : | : | : | : | : | : | : |
Oy 37 KTSKRRIVYDCTLEEKAYKSAKCSGEPSSSE--ENV-----DYFSAATNIPLEA 86
   1 : | | | | | : | : | : | : | : | : | : | : | : | : | : |
Db 97 RASNRKRYATYCEAKSAVESAKKQCTTASSWERYDENLVIEDPRDINHA-----LKA 151
   1 : | | | | | : | : | : | : | : | : | : | : | : | : | : |

```

OY 87 GNSWGEIPEL-----RKQVYNKNGKTSTIANMWDSHDLGCAVVDS--GRNHWCOYG 140  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
DB 152 IISWATEAFNLNKTKGBGVYRSILDISNFANLANMDREKVGACAVVKCSYPRTTHVCXP 211  
  
OY 141 PEAKGDGTIEEAGSPCSRSD 163  
::: || | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
DB 212 KKSRRKENPIYTGNRCGGGSDD 234

RESULT 23  
AAAY23608  
ID ID AMY23608 standard; Protein: 270 AA.

AC AAY23608;  
NC  
XX 03-SEP-1999 (first entry)  
DE Canine hookworm neutrophil inhibitory factor AcanNIF24 polypeptide.  
KM Neutrophil inhibitory factor: NfF mutant; shock; stroke;  
KM allergic rejection; vasculitis; autoimmune diabetes; AIDS;  
KM rheumatoid arthritis; inflammatory skin disease; myocardial infarction;  
KM inflammatory bowel disease; adult respiratory distress syndrome;  
KM ischemic reperfusion injury; acute inflammation; bacterial infection;  
KM vaccine; parasitic worm infection; antihelminthic.  
XZ Ancyllostoma caninum.  
OS  
XX US5919900-A..  
FN  
PD 06-JUL-1999.  
PF 26-MAY-1995; 95US-0450497.  
PR 23-DEC-1993; 93US-0173510.  
PR 11-MAY-1992; 92US-0881721.  
PR 24-DEC-1992; 92US-0996972.  
PR 11-MAY-1993; 93US-0060433.  
PR 10-NOV-1993; 93US-0151064.  
PR 26-MAY-1995; 95US-0450497.  
XX  
PA (CONV-) CORVAS INT INC.  
PX  
P1 Foster DL, Moyle M;  
DR WPI: 1999-403975/34.  
DR N-PDSB: AXM85545.  
XX  
PT Mutant Neutrophil Inhibitory Factors useful for treating  
PT inflammatory conditions and especially to prevent or decrease  
PT inflammatory responses  
PS  
PS Example 21: Flg 16A-V; 131pp: English.

The specification describes mutant Neutrophil Inhibitory Factors (NIFs), where at least 1 of the Asp residues at positions 18, 87, 110, 130, 187, or 223 in the wild type sequence (see AY23591) is replaced by a Glu residue. NIFs may be useful for treating shock, stroke, acute and chronic allograft rejection, vasculitis, autoimmune diabetes, rheumatoid arthritis, inflammatory skin diseases, inflammatory bowel disease, adult respiratory distress syndrome (ARDS), ischemia-reperfusion injury following myocardial infarction, and acute inflammation caused by bacterial infection such as sepsis or bacterial meningitis. NIFs or NIF fragments may be used as vaccines against parasitic worm infection. Anti-NIF antibodies may be useful for detecting infection of a mammalian host by a parasitic worm, as antihelminthic agents, and in the detection and isolation of NIF from tissue homogenates, cloned cells etc. NIFs may be useful for the detection of NIF mimics or antagonists in other compounds. Other NIF agonists and inhibitors may also be used as antihelminthic agents. MY23600-10 represent canine hookworm NIF proteins.

Sequence 270 AA:

RESULT 24  
MAY 22 6 03

AC MAY 23 602;

DE Canine hookworm neutrophil inhibitory factor PCR-NIF20 polypeptide  
XX

KW allograft rejection; vasculitis; autoimmune diabetes; APS-1  
 KM neutrophil inhibitory factor; NIF; mutant; shock; stroke;

**KW** Inflammatory bowel disease; adult respiratory distress syndrome:

vacine; parasitic worm infection; anthelmintic.

**Ancylostoma caninum.**

PN US5919900-A.  
XX

PD 06-JUL-1999.  
XX

FE 40-MAY-1995; 9505-0450497  
XX

PR	11-MAY-1992;	92US-0881721
EA	DEC-1993;	93US-0173310

PR 11-MAY-1993; 93US-0060433

PR 26-MAY-1995; 95US-0450497.

PA (CORV-) CORVAS INT INC.  
XY

PI Foster DL, Moyle M;  
XX

DR WPT; 1999-403975/34.  
DR N-PSDB; AAX85539.

PT	Mutant Neutrophil In
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**PT** Inflammatory response

PS Example 21; Flg 16A-

CC The specification de  
CC where at least 1 of

or 223 in the wild t  
residue NTFa may be

chronic allograft rejection, inflammation, arthritis, inflammatory

Query Match	27.08;	Score 269;	DB 20;	Length 263;
Best Local Similarity	32.28;	Pred. No. 1.6e-19;		
Matches	66;	Conservative	21;	Mismatches 58; Indels 60; Caps 6
14 DDDKEMETELHNGYRAAFARNY-----				-----KTSKRTWYVD 47
24 NDSIILQFLAHNGYSKLLALCHISITDESESDDEYDYWYAPYAPYAPYATSKRMRYLEYD 83				-----KTSKRTWYVD 47
48 CYLEEAKYKSAKSCSE--PSEEEENVDF-----				-----SAATLNIPLAGSNWSEFEL 97
84 CEAKRSAYMSRNCSSSPPEGYDENKRYFENSNINSEARLAI-----				-----LSNAKEAFD 138
98 -----RGKYKNNKNTNINMYWDSHDKLCAVYDC-----				-----SGKTHVYCO 138
139 NKTGCVLYVNSNLIITISNPLAMDIREKFGCAVYVNCPLDEIDADYDEBYATATIHVHC 198				-----SGKTHVYCO 138
139 YGPEAKGPGKTYEEGAPSRCSVD 163				-----SGKTHVYCO 138
199 IPRKMTGEPIYKVTGTPDQDSEI 223				-----SGKTHVYCO 138

RESULT 25  
AAR52988  
ID AAR52988 standard; Protein; 224 AA.

XX	AC	AA	AA
XX	AAR52988;		
XX	02-JUN-1994 (first entry)		
XX	Canine hookworm Neutrophil Inhibitory Factor isoform 3FL.		
XX	neutrophil inhibitory factor; NIF; glycoprotein; endoparasite;		
XX	parasitic worm; canine hookworm; peritoneal inflammation.		
XX	Ancylostoma caninum.		
XX	MO3232063-A.		
XX	25-NOV-1993.		
XX	11-MAY-1993; 93MO-US04502.		
XX	11-MAY-1992; 92US-0881721.		
XX	24-DEC-1992; 92US-0996972.		
XX	(CORV-) CORVAS INT INC.		
XX	Foster DL, Moyle M, Vlasuk GP;		
XX	WPI, 1993-386208/48.		
XX	New neutrophil inhibitory factor from parasitic worms - for		
XX	preventing and treating inflammation, also derived nucleic acid,		
XX	vectors, transformed hosts and antibodies		
XX	Example 10; Fig 9; 114pp: English.		
XX	A canine hookworm cDNA library was screened with a probe amplified		
XX	using primers 30.2 and 43.3.RC(AA052476 and AA052477, respectively)		
XX	which were based on sequences of isolated NIF peptide fragments. Seven		

which were based on sequences of isolated NIF peptide fragments. Seven

CC of the 120 positive clones were isolated for sequence analysis. One  
 CC isolate, designated clone 1FL, encoded an 825 nucleotide open reading  
 CC frame (AA032475). The other clones contained partial ORFs and encoded  
 CC partial NIF polypeptides (see AA032985-032990) which are thought to  
 CC represent six NIF isoforms that are significantly similar to, but  
 CC not identical to, the prototypical NIF-1FL polypeptide (AA032488).

XX Sequence 224 AA;

Query Match 26.7%; Score 266; DB 14; Length 224;  
 Best Local Similarity 33.8%; Pred. No. 2.7e-19;

Matches 66; Conservative 21; Mismatches 56; Indels 52; Gaps 7;

14 DDDREMFTELHNGYRAAFARNT-----KTSKRTMYDCT 49

31 NDSIRLQFLAMHNGYSKALGHISTDESESDDEYDWTAPAPTAASKRILEYDCE 90

50 LEEKAYSAKCE--EPSSSEENVDFSAATLNT---PLEAGSNWSEIFEL-----R 98

91 AEKSHMSARNCSDSSSPEDGDKYIFENSN-NISEBALAKAMISMAKAFNLKTEEGE 149

99 GAVTNKNGKTSNIANWVDSHDKLCAVVD-----SGKT-----HYVCOYGP 142

150 GVLIRSHNDISNFMALMDTRERKFCGAVVNCPLGEIDGTTIHGETYATTIHVCHYPM 209

143 AKGDGKIYEAGPC 157

210 NKTEGPIYKVKRKC 224

RESULT 26

AA032596

AA032596 standard; Protein: 224 AA.

AA032596;

03-SEP-1999 (first entry)

Canine hookworm neutrophil inhibitory factor isoform clone 4FL.

Neutrophil inhibitory factor; NIF; mutant; shock; stroke;

allergic rejection; vasculitis; autoimmune diabetes; ARDS;

rheumatoid arthritis; inflammatory skin disease; myocardial infarction;

inflammatory bowel disease; adult respiratory distress syndrome;

ischemia-reperfusion injury; acute inflammation; bacterial infection;

vaccine; parasitic worm infection; anthelmintic.

Ancylostoma caninum.

US5919900-A.

06-JUL-1999.

26-MAY-1995; 95US-0450497.

23-DEC-1993; 93US-0173510.

11-MAY-1993; 92US-0881721.

24-DEC-1992; 92US-0986972.

11-MAY-1993; 93US-0060433.

10-NOV-1993; 93US-0151064.

26-MAY-1995; 95US-0450497.

(CORV-) CORVAS INT INC.

Foster DL, Moyle M;

WPI; 1999-403975/34.

Mutant Neutrophil Inhibitory Factors useful for treating

inflammatory conditions and especially to prevent or decrease

inflammatory responses

Example 10; Fig 9A-E; 131pp; English.

XX The specification describes mutant Neutrophil Inhibitory Factors (NIFs),  
 CC where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197,  
 CC or 223 in the wild type sequence (see AA032591) is replaced by a Gln  
 CC residue. NIFs may be useful for treating shock, stroke, acute and  
 CC chronic allograft rejection, vasculitis, autoimmune diabetes, rheumatoid  
 CC arthritis, inflammatory skin diseases, inflammatory bowel disease, adult  
 CC respiratory distress syndrome (ARDS), ischemia-reperfusion injury  
 CC following myocardial infarction, and acute inflammation caused by  
 CC bacterial infection such as sepsis or bacterial meningitis. NIFs or NIF  
 CC fragments may be used as vaccines against parasitic worm infection.  
 CC Anti-NIF antibodies may be useful for detecting infection of mammalian  
 CC hosts by a parasitic worm, as anthelmintic agents, and in the detection  
 CC and isolation of NIF from tissue homogenates, cloned cells etc. NIFs may  
 CC be useful for the detection of NIF mimics or antagonists in other  
 CC compounds. Other NIF agonists and inhibitors may also be used as  
 CC anthelmintic agents. AA032592-98 represent isoform clones of canine  
 CC hookworm NIF.

XX Sequence 224 AA;

Query Match 26.7%; Score 266; DB 20; Length 224;  
 Best Local Similarity 33.8%; Pred. No. 2.7e-19;

Matches 66; Conservative 21; Mismatches 56; Indels 52; Gaps 7;

14 DDDREMFTELHNGYRAAFARNT-----KTSKRTMYDCT 49

31 NDSIRLQFLAMHNGYSKALGHISTDESESDDEYDWTAPAPTAASKRILEYDCE 90

50 LEEKAYSAKCE--EPSSSEENVDFSAATLNT---PLEAGSNWSEIFEL-----R 98

91 AEKSHMSARNCSDSSSPEDGDKYIFENSN-NISEBALAKAMISMAKAFNLKTEEGE 149

99 GAVTNKNGKTSNIANWVDSHDKLCAVVD-----SGKT-----HYVCOYGP 142

150 GVLIRSHNDISNFMALMDTRERKFCGAVVNCPLGEIDGTTIHGETYATTIHVCHYPM 209

143 AKGDGKIYEAGPC 157

210 NKTEGPIYKVKRKC 224

RESULT 27

AA04321

AA04321 standard; Protein: 424 AA.

AA04321;

17-JAN-1997 (first entry)

Ancylostoma secreted protein ASP-1 (pro-form).

Ancylostoma secreted protein; ASP-1; hookworm; vaccine.

Ancylostoma caninum.

Key Location/Qualifiers

Peptide 1..18

Protein /label= Sig-peptide

19..424

/label= Mat-protein

WO9632479-A1.

17-OCT-1996.

10-APR-1996; 96WO-US04821.

10-APR-1995; 95US-0419414.

(UTTA) UNIV YALE.

Hawdon JM, Hotez PJ, Jones BF;

DR WP1; 1996-477130/47.  
 DR N-PSDB; AAT38466.  
 XX Ancylostoma caninum secreted protein - useful as antigen for  
 PT hookworm vaccine prodn.  
 XX  
 XX Claim 2; Page 42-43; 66pp; English.  
 XX Ancylostoma secreted protein ASP-1 is secreted by canine hookworm  
 CC larvae as they change from the free-living stage to the parasitic  
 CC stage. The amino acid sequence of the ASP-1 pro-form (AAW04321) was  
 CC ded. from a cDNA clone (AAT38466) obtd. from an Ancylostoma caninum  
 CC L3 larvae cDNA library. ASP-1 represents a family of proteins (see  
 CC also AAW04322-23) that are highly immunogenic in experimental  
 CC animals. Recombinant ASP proteins can be produced in a variety of  
 CC hosts. They can be used in vaccines for hookworm, in the diagnosis  
 CC of hookworm infection, or to raise antibodies.  
 XX  
 SQ Sequence 424 AA; Score 265.5; DB 17; Length 424;  
 Query Match 36.6%; Best Local Similarity 32.5%; Pred. No. 7,4e-19;  
 Matches 62; Conservative 27; Mismatches 71; Indels 31; Gaps 6;  
 QY 7 COOREKLDMMREMFTELHNGYRAAFARNY-----KTSKMTVYDCTLEERKAYK 56  
 Db 227 CSPNNGMDSYRDFTLSVHNEFRSSVARGLEPDALGNAKRAKMLKMYDCEVASAIR 286  
 QY 57 SAEKSESESESESE---NDVPSAATLN-----PLEAGNSWMSRIF-----LRG 99  
 Db 287 HGKICYQHSHGEDRPGLEGNIKTYSVLKFDKNKAQAQSLMMNELKEFGVSPNVLT 346  
 QY 100 KYVNNKG--KTSNINAMWDSHDKLGCAVYDCSGKTHVVCQYCPKAGDCKTIEGAPCS 158  
 Db 347 ALMNRGQIGHTYGMAMDTYTLGCAVYFCNDFFVCGYCPGNGMGMHYITWGGCS 406  
 QY 159 RGSDDYAGAYTC 169  
 Db 407 QCS---PGATC 414  
 RESULT 28  
 AAW04322  
 ID AAW04322 standard; Protein; 218 AA.  
 AC AAW04322;  
 XX 17-JAN-1997 (first entry)  
 DE Ancylostoma secreted protein ASP-2 type I.  
 XX Ancylostoma secreted protein; ASP-2; hookworm; vaccine.  
 KW Ancylostoma caninum.  
 OS Ancylostoma caninum.  
 XX WO9632479-A1.  
 PN 17-OCT-1996.  
 PD 10-APR-1996; 96WO-US04821.  
 PF 10-APR-1995; 95US-0419414.  
 PR 10-APR-1995; 95US-0419414.  
 XX (UYVA ) UNIV YALE.  
 PA Hawdon JM, Hotez PJ, Jones BF;  
 XX WPI; 1996-477130/47.  
 DR N-PSDB; AAT38467.  
 XX Ancylostoma caninum secreted protein - useful as antigen for  
 PT hookworm vaccine prodn.

XX Claim 2; Page 49-50; 66pp; English.  
 PS Ancylostoma secreted protein ASP-2 type I (AAW04322) is secreted by  
 XX canine hookworm larvae as they begin feeding. Its amino acid  
 CC sequence was deduced from a cDNA clone (AAT38467) isolated from an  
 CC Ancylostoma caninum L3 larvae cDNA library. Type I ASP-2 differs  
 CC from type II ASP-2 (AAW04323) only in amino acid positions 92 and 95.  
 CC The proteins are members of a family of proteins (see also AAW04321)  
 CC that are highly immunogenic in experimental animals. Recombinant  
 CC ASP proteins can be produced in a variety of hosts. They can be  
 CC used in vaccines for hookworm in the diagnosis of hookworm  
 CC infection, or to raise antibodies.  
 XX  
 SQ Sequence 218 AA; Score 262; DB 17; Length 218;  
 Query Match 26.3%; Best Local Similarity 30.4%; Pred. No. 6,7e-19;  
 Matches 58; Conservative 38; Mismatches 69; Indels 26; Gaps 5;  
 QY 13 LDDDMREMFTELHNGYRAAFARNY-----KTSKMTVYDCTLEERKAYKSAKCS 62  
 Db 27 WMDERAKKFLDVHNSRSMVAKGAKOAKISGNAPKAKKKKMIYDCHNESTAMONARKCV 86  
 QY 63 EEPSSSE---ENDVPSAATLN-----PLEAGNSWMSRIF-----ELRGKYNNKNGKT 108  
 Db 87 FAHSRRGQVGENIMWSTARQMDKAQAQASDGFSESLAKYGVGOENKLTJOLNRRGVMI 146  
 QY 109 SNIAWVWDSHDKLGCAVYDCSGKTHVVCQYCPKAGDCKTIEGAPCSRSDYAGAYT 168  
 Db 147 GHYTMWQWSEYKLGCVEMCSTMVYGVCGYSPGNNMMSLIYERGNPCTKSDSGSNAS 206  
 QY 169 CPDDWQNLICI 179  
 Db 207 CSAG--EALCY 215  
 RESULT 29  
 AAW04323  
 ID AAW04323 standard; Protein; 218 AA.  
 AC AAW04323;  
 XX 17-JAN-1997 (first entry)  
 DE Ancylostoma secreted protein ASP-2 type II.  
 XX Ancylostoma secreted protein; ASP-2; hookworm; vaccine.  
 KW Ancylostoma caninum.  
 OS Ancylostoma caninum.  
 XX WO9632479-A1.  
 PN 17-OCT-1996.  
 PD 10-APR-1996; 96WO-US04821.  
 PF 10-APR-1995; 95US-0419414.  
 PR 10-APR-1995; 95US-0419414.  
 XX (UYVA ) UNIV YALE.  
 PA Hawdon JM, Hotez PJ, Jones BF;  
 XX WPI; 1996-477130/47.  
 DR N-PSDB; AAT38468.  
 XX Ancylostoma caninum secreted protein - useful as antigen for  
 PT hookworm vaccine prodn.  
 XX Claim 2; Page 51; 66pp; English.  
 PS Ancylostoma secreted protein ASP-2 type II (AAW04323) is secreted by  
 CC canine hookworm larvae as they begin feeding. Its amino acid



PT vectors, transformed hosts and antibodies  
 XX Example 10; Fig 9; 114pp; English.  
 CC A canine hookworm cDNA library was screened with a probe amplified  
 CC using primers 30.2 and 43.3.RC(AA052476 and AA052477, respectively)  
 CC which were based on sequences of isolated NIF peptide fragments. Seven  
 CC of the 120 positive clones were isolated for sequence analysis. One  
 CC isolate, designated clone 1FL, encoded an 825 nucleotide open reading  
 CC frame (AA052475). The other clones contained partial ORFs and encoded  
 CC partial NIF polypeptides (see AA052985-R52990) which are thought to  
 CC represent six NIF isoforms that are significantly similar to, but  
 CC not identical to, the prototypical NIF-1FL polypeptide (AA042488).  
 XX Sequence 208 AA;  
 SQ  
 Query Match 25.6%; Score 255; DB 14; Length 208;  
 Best Local Similarity 36.5%; Pred. No. 3.3e-18;  
 Matches 65; Conservative 18; Mismatches 55; Indels 40; Gaps 8;  
 OY 14 DDDMRMFTLHNGRAFAFARY--KTSKMTMYDCTLEKAYKSAKNC--SEEPSSE 68  
 DB 3 DDD-----YEGFLPDFAPRASKMRYLEDCAEKSAVVSANCSNISPPEG 51  
 OY 69 EENVDFSAATLNI---PLEAGSNWSEIFEL---RGKYNNKNGKTSNINAMVWDSHDK 121  
 DB 52 DENKIYFENSN-NISEBAKAMISWAKENFNLKTGEGVLYRSLTISFALAMDTRK 110  
 OY 122 LGCAVVDGS-GK-----THVCOYGPBAKGDKTYIEBGAFCRSRSDY 163  
 DB 111 FGCAYVNCPLGKPDALITDDEENYATRAIHVCHYKPKIKTGEQPIYKVGPCDDCSEY 168  
 RESULT 32  
 AA052594  
 ID AA052594 standard; Protein; 208 AA.  
 XX  
 AC AA052594;  
 DT 03-SEP-1999 (first entry)  
 XX  
 DE Canine hookworm neutrophil inhibitory factor isoform clone 2FL.  
 XX  
 KW Neutrophil inhibitory factor; NIF; mutant; shock; stroke;  
 KW allograft rejection; vasculitis; autoimmune diabetes; ARDS;  
 KW rheumatoid arthritis; inflammatory skin disease; myocardial infarction;  
 KW inflammatory bowel disease; adult respiratory distress syndrome;  
 KW ischemia-reperfusion injury; acute inflammation; bacterial infection;  
 KW vaccine; parasitic worm infection; antihelminic.  
 XX  
 OS Ancylostoma caninum.  
 OS  
 PN US919900-A.  
 XX  
 PD 06-JUL-1999.  
 XX  
 PP 26-MAY-1995; 95US-0450497.  
 XX  
 PR 23-DEC-1993; 93US-0173510.  
 PR 11-MAY-1992; 92US-0881721.  
 PR 24-DEC-1992; 92US-0996972.  
 PR 11-MAY-1993; 93US-0060433.  
 PR 10-NOV-1993; 93US-0151064.  
 PR 26-MAY-1995; 95US-0450497.  
 XX  
 PA (CORV-) CORVAS INT INC.  
 XX  
 PI Foster DL, Moyle M;  
 XX  
 DR WPI; 1999-403975/34.  
 XX  
 PT Mutant Neutrophil Inhibitory Factors useful for treating  
 PT inflammatory conditions and especially to prevent or decrease

PT inflammatory responses  
 XX Example 10; Fig 9A-E; 131pp; English.  
 XX  
 CC The specification describes mutant Neutrophil Inhibitory Factors (NIFs),  
 CC where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197,  
 CC or 223 in the wild type sequence (see AA052591) is replaced by a Glu  
 CC residue. NIFs may be useful for treating shock, stroke, acute and  
 CC chronic allograft rejection, vasculitis, autoimmune diabetes, rheumatoid  
 CC arthritis, inflammatory skin diseases, inflammation, bowel disease, adult  
 CC respiratory distress syndrome (ARDS), ischemia-reperfusion injury  
 CC following myocardial infarction, and acute inflammation caused by  
 CC bacterial infection such as sepsis or bacterial meningitis. NIFs or NIF  
 CC fragments may be used as vaccines against parasitic worm infection.  
 CC Anti-NIF antibodies may be useful for detecting infection of a mammalian  
 CC host by a parasitic worm, as antihelminic agents, and in the detection  
 CC and isolation of NIF from tissue homogenates, cloned cells etc. NIFs may  
 CC be useful for the detection of NIF mimics or antagonists in other  
 CC compounds. Other NIF agonists and inhibitors may also be used as  
 CC antihelminic agents. AA052592-98 represent isoform clones of canine  
 CC hookworm NIF.  
 XX  
 SQ  
 Sequence 208 AA;  
 Query Match 25.6%; Score 255; DB 20; Length 208;  
 Best Local Similarity 36.5%; Pred. No. 3.3e-18;  
 Matches 65; Conservative 18; Mismatches 55; Indels 40; Gaps 8;  
 OY 14 DDDMRMFTLHNGRAFAFARY--KTSKMTMYDCTLEKAYKSAKNC--SEEPSSE 68  
 DB 3 DDD-----YEGFLPDFAPRASKMRYLEDCAEKSAVVSANCSNISPPEG 51  
 OY 69 EENVDFSAATLNI---PLEAGSNWSEIFEL---RGKYNNKNGKTSNINAMVWDSHDK 121  
 DB 52 DENKIYFENSN-NISEBAKAMISWAKENFNLKTGEGVLYRSLTISFALAMDTRK 110  
 OY 122 LGCAVVDGS-GK-----THVCOYGPBAKGDKTYIEBGAFCRSRSDY 163  
 DB 111 FGCAYVNCPLGKPDALITDDEENYATRAIHVCHYKPKIKTGEQPIYKVGPCDDCSEY 168  
 RESULT 33  
 AA0537166  
 ID AA0537166 standard; Protein; 222 AA.  
 XX  
 AC AA0537166;  
 DT 06-JUL-1998 (first entry)  
 XX  
 DE Haemonchus contortus ES24 antigen.  
 XX  
 KW ES24; antigen; excretory secretory trichostrongylid protein;  
 KW diarrhoea; anaemia; gastro-intestinal nematode; vaccine; sheep;  
 KW goat.  
 XX  
 OS Haemonchus contortus.  
 OS  
 PN  
 PD 15-JAN-1998.  
 XX  
 PP 04-JUL-1997; 97WO-NL00380.  
 XX  
 PR 04-JUL-1996; 96EP-0201856.  
 XX  
 FT Key Location/Qualifiers  
 FT Peptide 1..19  
 FT Protein /Label-Sig\_peptide  
 FT 20..222  
 FT /Label-Mat\_protein  
 FT 114..116  
 FT /note="Asn is N-glycosylated"

PA (UYUT-) RIKSUNIV UTRICHT.  
 XX PI Cornelissen AMCA, Schallig HDEH;  
 XX WPI: 1998-101048/09.  
 DR N-PSDB; AAV03016.  
 XX Polynucleotide encoding excretory secretory trichostrongylid  
 PT proteins - ES15 or ES24 of Haemonchus contortus or ES14.0 or ES14.2  
 PT of Cooperia oncophora, useful for vaccines against gastro-intestinal  
 PT nematodes  
 XX  
 PS Claim 5; Page 26; 42pp; English.  
 XX  
 CC This polypeptide comprises the excretory secretory (ES)  
 CC trichostrongylid protein ES24 of the gastro-intestinal nematode  
 CC Haemonchus contortus. Its amino acid sequence was deduced from a  
 CC cDNA clone (see AAV03016) isolated from an L3 larval cDNA library.  
 CC Also claimed is a recombinant ES24 polynucleotide comprised in  
 CC a vector, and a vaccine for combating H. contortus infections in  
 CC sheep or goats that comprises the recombinant polynucleotide or the  
 CC ES24 protein. Vaccines are also provided that contain or express  
 CC the ES15 protein (see AAV37165) of H. contortus or the ES14.0 (see  
 CC AAV37167) or ES14.2 (see AAV37168) antigen of Cooperia oncophora.  
 CC Trichostrongylids are a major constraint in ruminant production  
 CC world-wide, e.g. producing diarrhoea or anaemia leading to reduced  
 CC milk, meat and wool production. To enhance immunogenicity, the ES  
 CC polypeptides can be used as homopolymers, hetero-polymers, or  
 CC coupled with other compounds, e.g. adjuvants.  
 XX  
 SO Sequence 222 AA;  
 Query Match 21.5%; Score 214; DB 19; Length 222;  
 Best Local Similarity 28.0%; Pred. No. 6.6e-14;  
 Matches 58; Conservative 28; Mismatches 89; Indels 32; Gaps 8;  
 QY 2 GDYSICQOREKLDNREKFTELHNGYRAAFARY-----KTSKRTMYDCT 49  
 DB 17 GIASACDPDTGMSDEVRQTFVKNHNAVYTLVAKGKRNKEIGYAPPAAMLYKVVDA 76  
 QY 50 LEENAYSAKRC--SEEPSSEEN--VDVPSAATLN-----IPLDAGNSWSEIFELRCK 100  
 DB 77 IEEHTMFAKCVFAHNSYSESNMGNOMLYTWTSLNQNTVAALSDVLMFDEL--QONGCV 135  
 QY 101 VYNR-----NGKTSINIANVWDSHDLGCAVVDSCGKTHVVCYGEPAKGDGKTYEE 153  
 DB 136 PDIYNTMVAVFNRGVGHYQVWQMSNKGICAVEMCSDMTFVACEDSAGVYGMPIYEV 195  
 QY 154 GAPCRCSDYG-AGVYCDDDMONLICI 179  
 DB 196 GNPCTNEDCKCTNCYCSRD--EALCI 220  
 RESULT 34  
 ID AAR26785 standard; Protein; 454 AA.  
 AC AAR26785;  
 XX 26-JAN-1993 (first entry)  
 DE Sequence of a homologue of the 45 kd antigen encoded by  
 DE pBTA879.  
 XX Antigen; vaccine; parasitic nematode; immunogen.  
 XX Haemonchus contortus.  
 OS  
 XX Key Location/Qualifiers  
 FH 22..42  
 FT Region /note- "homologous to 45 kd protein"  
 FT 253..273  
 FT /note- "see above"

FT Region 274..287  
 FT /note- "homologous with Endoprotease Lys-C  
 FT peptide"  
 FT 302..0  
 FT Region /note- "as above"  
 XX  
 PN W09213889-A.  
 XX  
 PD 20-AUG-1992.  
 XX  
 PE 06-FEB-1992; 92MO-AU000040.  
 XX  
 PR 06-FEB-1991; 91AU-0004486.  
 XX  
 PA (BIOT-) BIOTEC AUSTRALIA PTY LTD.  
 XX  
 PI Cobon GS, Sharp PJ, Wagland BM;  
 XX WPI: 1992-289990/36.  
 DR N-PSDB; AAQ28093.  
 XX  
 PT Vaccines comprise antigens derived from parasitic nematodes -  
 PT useful for passive immunisation against round, whip, filarities,  
 PT thread and hookworms on host  
 XX  
 PS Claim 15; Fig 7; 86pp; English.  
 XX  
 CC PCR primers A112/301 and A112/302 were designed to be used to  
 CC amplify the DNA encoding the 45 kd protein. In the reaction  
 CC containing primer A112/301 a unique band of approximately 650 bp was  
 CC observed. The approximately 650 bp band was not seen when primer  
 CC A112/302 was used. The PCR cloned was grown and purified for use as  
 CC a hybridisation probe to screen the pBTA879 cDNA library. pBTA879  
 CC is the sequence of one of these clones. There is no methionine  
 CC initiation codon present in this region of the sequence so this clone  
 CC probably does not represent the complete coding region. pBTA879  
 CC identical to, the native glycoprotein which is related to, but not  
 CC identical to, the native glycoprotein isolated from H. contortus.  
 CC In order to isolate a cDNA clone coding for the full length native  
 CC 45 kd antigen, cDNA libraries were screened with the fragment  
 CC isolated from pBTA879. AAQ28094 is the sequence of one of these  
 CC clones, pBTA 953. Once again, this clone does not contain an  
 CC initiation methionine.  
 XX  
 SO Sequence 454 AA;  
 Query Match 20.6%; Score 205; DB 13; Length 454;  
 Best Local Similarity 28.5%; Pred. No. 1.6e-12;  
 Matches 55; Conservative 36; Mismatches 74; Indels 28; Gaps 8;  
 QY 13 LDDNREKFTELHNGYRAAFARY-----KTSKRTMYOCTLEKAYSAKCS 62  
 DB 262 MTDKARKFTVDKHEHYSILAKQAKGKPGAPAKAABAKAYITDCEVANMEKTCI 321  
 QY 63 EEPSSSE-----ENVVPSAATLN-----IPLDAGNSWSEIFEL--RGRYYNNGKT-- 108  
 DB 322 FGLNTAMALKRGNMNMSSKANNTETAALAEAVAAWFGDLQRYGVPENNVFTMNVTTL 381  
 QY 109 SNIANNVWDSHDLGCAVYDC-SGKTHVVCYGEPAKGDGKTYEAGPACSCSDYGA-G 166  
 DB 382 SKYSQLAWQSSDRIGCVAVPCWMSWTVVACETNPGDLPALYDVGDCYKADCCOPG 441  
 QY 167 VYCDDDMONLICI 179  
 DB 442 CTCRSR--EGLCV 452  
 RESULT 35  
 ID AAR26786 standard; Protein; 440 AA.  
 AC AAR26786;  
 XX AAR26786;



XX	PT	26-JAN-1993 (first entry)
XX	DE	Sequence of a homologue of the 45 kD antigen encoded by pBR863.
XX	OS	Antigen; vaccine; parasitic nematode; immunogen.
XX	XN	Hemonchus contortus.
FH	FH	Key Location/Qualifiers
FT	FT	Region 12..31 /note= "homologous to 45 kD protein"
FT	FT	Region 237..256 /note= "see above"
XX	PX	M09213889-A.
XX	PD	20-AUG-1992.
XX	PE	06-FEB-1992; 92MO-AU00040.
XX	PR	06-FEB-1991; 91AU-0004486.
XX	PA	(BIOT-) BIOTECH AUSTRALIA PTY LTD.
PI	PI	Cobon GS, Sharp PJ, Wagland BM;
DR	N-PDSB	WPI; 1992-289990/36. N-PDSB; AAQ28094.
XX	PT	Vaccines comprise antigens derived from parasitic nematodes - useful for passive immunisation against round, whip, filariae,
XX	PT	thread and hookworms on host
XX	XX	Claim 11; Fig 8; 86pp; English.
XX	CC	PCR primers A112/301 and A112/302 were designed to be used to amplify the DNA encoding the 45 kD protein. In the reaction containing primer A112/301 a unique band of approximately 650 bp was observed. The PCR cloned was grown and purified for use as A112/302 was used. The PCR cloned was grown and purified for use as a hybridisation probe to screen the pBR879 cDNA library. pBR879 is the sequence of one of these clones. There is no methionine initiation codon present in this region of the sequence so this clone probably encodes a glycoprotein which is related to, but not identical to, the native glycoprotein isolated from H. contortus. In order to isolate a cDNA clone coding for the full length native 45 kD antigen cDNA libraries were screened with the fragment isolated from pBR879. AAQ28094 is the sequence of one of these clones pBR 963. Once again, this clone does not contain an initiation methionine.
XX	CC	Sequence 440 AA;
DG	XX	Score 20.2%; Score 201; DB 13; Length 440; Best local Similarity 26.8%; Pred. No. 4e-12; Indels 70; Gaps 7 Matches 56; Conservative 23; Mismatches 60;
OY	DB	13 LDDDKREKFELINGRAFAFRNY-----FTSKARTMYIDCTLEAKYSARKS 62   :   :   :   :   :   :   :   :   :   :   :   :   :   :   21 MDDELRIQFVDKHEFYRSILINQAKKRKGAFAPKARMLVIGDCVEANTAAAYADCK 80   :   :   :   :   :   :   :   :   :   :   :   :   :   :   OY 63 EEPSESEENVDFSAATLIPLEGNSMWSGEIFELRGRYNK--NGTFS ----- 109   :   :   :   :   :   :   :   :   :   :   :   :   :   :   DB 81 FE-----HDPEORNRNTMGNIIMLGITWTSTESALSYQAMYTELMKF 124   :   :   :   :   :   :   :   :   :   :   :   :   :   :   OY 110 ----NIAM----VWDSDRLCAVYDSCGRTHYCOYGPKAGDGOKTY 151   :   :   :   :   :   :   :   :   :   :   :   :   :   :   DB 125 GVDEDMITIMEFDVGRTGYAVTAOAQSSDKICGAEMCEPMTLVACEIYNAGRIRNHII 184   :   :   :   :   :   :   :   :   :   :   :   :   :   :   OY 152 EGAPCSRCSDYGAGVTCDDDQNQLCTIG 180   :   :   :   :   :   :   :   :   :   :   :   :   :   :

	DB	.185 DIGDPC-----TTDEDMO---CTG 200
	RESULT 36	
	AAR52990	
	AAR52990 standard; Protein: 189 AA.	
XX	AAAR52990;	
XX	02-JUN-1994 (first entry)	
XX	Canine hookworm Neutrophil inhibitory factor isoform 6FL.	
DE	neutrophil inhibitory factor; NIF; glycoprotein; endoparasite;	
KW	nematode; parasitic worm; canine hookworm; peritoneal inflammation.	
OS	Ancylostoma caninum.	
XX	M09323063-A.	
PX	PN	
XX	25-NOV-1993.	
PF	11-MAY-1993; 93WO-0504502.	
XX	PR 11-MAY-1992; 92US-0881721.	
PR	24-DEC-1992; 92US-0936972.	
PA	(CORV-) CORVAS INT INC.	
PI	Foster DL, Moyle M, Vlasuk GP;	
DR	WPI: 1993-386208/48.	
XX	New neutrophil inhibitory factor from parasitic worms - for preventing and treating inflammation, also derived nucleic acid, vectors, transformed hosts and antibodies	
PS	Example 10; Fig 9; 11app; English.	
CC	A canine hookworm cDNA library was screened with a probe amplified	
CC	which primers 30.2 and 43.3.RC(AA052476 and AA052477, respectively)	
CC	of the 120 positive clones were isolated for sequence analysis. Seven	
CC	clones designated clone 1FL, encoded an 825 nucleotide open reading	
CC	frame (AA052475). The other clones contained partial ORFs and coded	
CC	partial NIF polypeptides (see AAR52985-R32990) which are thought to	
CC	represent six NIF isoforms that are significantly similar, but	
CC	not identical to, the prototypical NIF-1FL polypeptide (AAR52488).	
SO	Sequence 189 AA:	
	Query Match 20.1%; Score 200; DB 14; Length 189;	
	Best Local Similarity 32.9%; Pred. No.1,5e-12; Indels 40; Gaps 6;	
	Matches 50; Conservative .16; Mismatches 46;	
OY	15 DMRBMETELHNGCYRAAFARNY-----KTSKKRPMVVDCT 49     :   :       : :	:
Dd	40 DSIRLOPFLAHNIGSRNLALGHGISGESIGDDYDDYYRYSSAPMKSRRYLEDCD 99   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :	:
OY	50 LEEKAAYSAEKCESE--PSEEDNDVF-SATATINIDLEGN---SWSSTFPL---- 97   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :	:
Dd	100 SESMSVMASNSCSUSSPEEGIDEKYILSNSNIN---EAERLAISGKEAFEMLNETG 156   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :	:
OY	98 RGVRYNKNGKTSNTANWWDSDHDICGAAYDC 129   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :	:
Dd	157 EGVLYRSNLTITSNFNLANLDREKRCGCAVVKC 188   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :	:
	RESULT 37	
	AAIY3598	
ID	AAIY3598 standard; Protein: 189 AA.	
XX	AAIY3598;	







Db	153	NPFCPRCSGPV-----CTHYOVVMTSNRIQCAINLCHNMNIWQIMPKAVYLVCNY	206
Oy	140	GPEAKDGKTIYEGAGCSRC-SDYGAG 166	
Db	207	SPKGNMWHGAPYKRGRCSCSPPSFGG 234	
	RESULT 42		
AA	AAAM39716		
XX	ID	AAAM39716 standard; Protein: 266 AA.	
XX	AC	AAAM39716;	
XX	DT	22-OCT-2001 (first entry)	
XX	DE	Human polypeptide SEQ ID NO 2861.	
XX	XX		
XX	XX	Human; nocitropic; immunosuppressant; cytostatic; gene therapy; cancer;	
XX	XX	peripheral nervous system; neuropathy; central nervous system; CNS;	
XX	XX	Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;	
XX	XX	amyotrophic lateral sclerosis; Shy-Drager Syndrome; Chemotactic;	
XX	XX	chemokine; thrombolytic; drug screening; arthritis; inflammation;	
XX	XX	Leukemia.	
XX	OS	Homo sapiens.	
XX	XX	MO200153312-A1.	
XX	XX	26-JUL-2001.	
XX	XX	26-DEC-2000; 2000WO-US34263.	
XX	XX	21-JAN-2000; 2000US-0488725.	
XX	XX	25-APR-2000; 2000US-0552317.	
XX	XX	09-JUL-2000; 2000US-0596042.	
XX	XX	19-JUL-2000; 2000US-0620312.	
XX	XX	03-AUG-2000; 2000US-0653450.	
XX	XX	14-SEP-2000; 2000US-0662191.	
XX	XX	19-OCT-2000; 2000US-0693036.	
XX	XX	29-NOV-2000; 2000US-0727344.	
XX	XX	(HYSE-) HXSDQ INC.	
XX	XX	Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;	
XX	XX	Wang J, Wang Z, Weinman T, Xu C, Xue AD, Yang Y, Zhang J;	
XX	XX	Zhao QN, Zhou P, Goodrich R, Dimaanic RT;	
XX	XX	WPI: 2001-442253/47.	
XX	XX	N-PSDB: AA158872.	
XX	XX	Novel nucleic acids and polypeptides, useful for treating disorders	
XX	XX	such as central nervous system injuries -	
XX	XX	Example 4: SEQ ID NO 2861; 10078pp; English.	
XX	XX	The invention relates to human nucleic acids (AA157798-AA161369) and	
XX	XX	the encoded polypeptides (AAAM38642-AAAM42213) with nocitropic,	
XX	XX	immunosuppressant and cytostatic activity. The polynucleotides are useful	
XX	XX	in gene therapy. A composition containing a polypeptide or polynucleotide	
XX	XX	of the invention may be used to treat diseases of the peripheral nervous	
XX	XX	system, such as peripheral nervous injuries, peripheral neuropathy and	
XX	XX	localised neuropathies and central nervous system diseases, such as	
XX	XX	Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic	
XX	XX	lateral sclerosis, and Shy-Drager Syndrome. Other uses include the	
XX	XX	utilisation of the activities such as: immune system suppression,	
XX	XX	Activin/Inhibin activity, chemotactic/chemokinetic activity, haemostatic	
XX	XX	and thrombolytic activity, cancer diagnosis and therapy, drug screening,	
XX	XX	assays for receptor activity, arthritis and inflammation, leukemias and	
XX	XX	C.N.S. disorders.	
XX	XX	Note: The sequence data for this patent did not form part of the printed	
XX	XX	specification.	

SQ Sequence 266 AA;  
 Query Match 15.9%; Score 159; DB 22; Length 266;  
 Best Local Similarity 28.6%; Pred. No. 4,5e-08;  
 Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;

Qy	13	LDMMRMFELTNGYRAAFANRKTSMPTMYDCTLEEKVSAEK-----SEPSSE	68
Db	28	LTDEKRLAMELHNLRYAQSPT--ADMDLHMKDEDLAFAKAYANOCYWGINKRGRR	85
Qy	69	EENDVYSATLTINPLEAGNSWSEIIEELGKRYNKNKSTSIANM-----YPSHDK	121
Db	86	GENLFAITDGMDFL-ANEEHNE-----REHYNLNATCSPOGOGCHTQYVWAKTER	139
Qy	122	LGCAVNDCS-----GRTAV---VCQYGPFAKGDGKTIYBEGAPCSRSDYGACVTCDDW	173
Db	140	IGCSHCEKMLQGVETNIEILVNCNTEPENVNGKRPYEGPCSCPC---SSQHC----	192
Qy	174	ONLIC 178	
Db	193	RNSLC 197	

RESULT 43  
 AAM41502  
 ID AAM41502 standard; Protein; 347 AA.  
 AC AAM41502;  
 XX  
 XX 22-OCT-2001 (first entry)  
 XX  
 DE Human polypeptide SEQ ID NO 6433.  
 XX  
 KW Human; nocitropic; immunosuppressant; cytostatic; gene therapy; cancer;  
 KW peripheral nervous system; neuropathy; central nervous system; CNS;  
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;  
 KW amyotrophic lateral sclerosis; Shy-Prager Syndrome; chemotactic;  
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;  
 KW leukemia.  
 KW  
 KW Homo sapiens.  
 OS  
 FN WO200153312-A1.  
 PN  
 PD 26-JUL-2001.  
 XX  
 PF 26-DEC-2000; 2000MO-DS34263.  
 XX  
 XX 21-JAN-2000; 2000US-0488725.  
 XX 25-APR-2000; 2000US-0552317.  
 XX 09-JUL-2000; 2000US-0598042.  
 XX 19-JUL-2000; 2000US-0620312.  
 XX 03-AUG-2000; 2000US-0653450.  
 XX 14-SEP-2000; 2000US-0662191.  
 XX 19-OCT-2000; 2000US-0693036.  
 XX 29-NOV-2000; 2000US-0727344.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
 XX Wang J, Wang Z, Weinman T, Xu C, Xue AJ, Yang Y, Zhang J;  
 PI Zhao Q, Zhou F, Goodrich R, Drmanac RJ;  
 DR WPI, 2001-442253/47.  
 DR N-PSDB: AAI60638.  
 XX  
 PT Novel nucleic acids and polypeptides, useful for treating disorders  
 XX such as central nervous system injuries -  
 XX Example 2; SEQ ID NO 6433; 10078bp; English.  
 XX  
 CC The invention relates to human nucleic acids (AA157798-AA161369) and  
 CC the encoded polypeptides (AAM38642-AAM42213) with nocitropic,

CC immunosuppressant and cytostatic activity. The polynucleotides are useful  
 CC in gene therapy. A composition containing a polypeptide or polynucleotide  
 CC of the invention may be used to treat diseases of the peripheral nervous  
 CC system, such as peripheral nervous injuries, peripheral neuropathy and  
 CC localised neuropathies and central nervous system diseases, such as  
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the  
 CC utilisation of the activities such as: Immune system suppression,  
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic  
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening  
 CC assays for receptor activity, arthritis and inflammation, leukemias and  
 CC C.N.S disorders.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification.

XX Sequence 347 AA:

Query Match 15.98; Score 159; DB 22; Length 347;  
 Best Local Similarity 28.68; Pred. No. 6.5e-08;  
 Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;

DB 13 LDDDMEMETELHNGVGAAPAFARYKSKRMVYDCLEKAKSKERC---SEEPSSE 68  
 DB 105 LTDEERKLVNELHLYRQVSPF--ASDMLHMDDELAFAPAYARQVGHNRKGR 162  
 OY 69 EENVDVFSALNTPIERAGNSWSEIFELRGVYTKNGKTSNIAM-----VWDSHK 121  
 DB 163 GEMFATIDEGMDVPL-AMEEMHE-----KEHMLSAICSFGQCGHYTVWAKTER 216  
 OY 122 LGCAYVDCS-----GKTHV---VCOYGPACKDGKTIYEGARCSGSGYGVTCDDW 173  
 DB 217 IGGGSHFCKLQGVDETRNLVCEHPEGNVKGRRPQKPCSCCP---SGHHC----- 269  
 OY 174 QNLIC 178  
 DB 270 KNSLC 274

# RESULT 44

AA113392  
 ID AA113392; standard; Protein: 463 AA.

XX AA113392;

XX 25-JUN-1999 (first entry)

XX Amino acid sequence of protein PRO328.

XX Secreted protein; transmembrane protein; human; enterocolitis;  
 KW Zollinger-Ellison syndrome; gastrointestinal ulceration;  
 KW congenital microvillus atrophy; skin disease; cell growth;  
 KW abnormal keratinocyte differentiation; psoriasis; epithelial cancer;  
 KW Parkinson's disease; Alzheimer's disease; ALS; neuropathy;  
 KW fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata;  
 KW anti-thrombotic; wound healing; tissue repair.

XX Homo sapiens.

XX MO9914328-A2.

XX 25-MAR-1999.

XX 16-SEP-1998; 98WO-0519330.

XX 25-NOV-1997; 97US-0066840.

XX 17-SEP-1997; 97US-0059113.

XX 17-SEP-1997; 97US-0059115.

XX 17-SEP-1997; 97US-0059117.

XX 17-SEP-1997; 97US-0059119.

XX 17-SEP-1997; 97US-0059121.

XX 17-SEP-1997; 97US-0059122.

XX 17-SEP-1997; 97US-0059184.

XX 18-SEP-1997; 97US-0059263.

PR 18-SEP-1997; 97US-0059266.  
 PR 15-OCT-1997; 97US-0062125.  
 PR 17-OCT-1997; 97US-0062285.  
 PR 17-OCT-1997; 97US-0062287.  
 PR 21-OCT-1997; 97US-0062486.  
 PR 24-OCT-1997; 97US-0062814.  
 PR 24-OCT-1997; 97US-0062816.  
 PR 24-OCT-1997; 97US-0063045.  
 PR 24-OCT-1997; 97US-0063120.  
 PR 24-OCT-1997; 97US-0063121.  
 PR 24-OCT-1997; 97US-0063128.  
 PR 27-OCT-1997; 97US-0063329.  
 PR 27-OCT-1997; 97US-0063541.  
 PR 28-OCT-1997; 97US-0063542.  
 PR 28-OCT-1997; 97US-0063544.  
 PR 28-OCT-1997; 97US-0063549.  
 PR 28-OCT-1997; 97US-0063550.  
 PR 28-OCT-1997; 97US-0063564.  
 PR 29-OCT-1997; 97US-0063435.  
 PR 29-OCT-1997; 97US-0063704.  
 PR 29-OCT-1997; 97US-0063732.  
 PR 29-OCT-1997; 97US-0063738.  
 PR 29-OCT-1997; 97US-0063739.  
 PR 29-OCT-1997; 97US-0063739.  
 PR 29-OCT-1997; 97US-0063739.  
 PR 31-OCT-1997; 97US-0063739.  
 PR 31-OCT-1997; 97US-0063739.  
 PR 03-NOV-1997; 97US-0064248.  
 PR 07-NOV-1997; 97US-0064809.  
 PR 12-NOV-1997; 97US-0065186.  
 PR 17-NOV-1997; 97US-0065846.  
 PR 18-NOV-1997; 97US-0065939.  
 PR 21-NOV-1997; 97US-0066120.  
 PR 21-NOV-1997; 97US-0066364.  
 PR 24-NOV-1997; 97US-0066772.  
 PR 24-NOV-1997; 97US-0066466.  
 PR 24-NOV-1997; 97US-0066770.  
 PR 24-NOV-1997; 97US-0066511.  
 PR 24-NOV-1997; 97US-0066453.

(GENTH ) GENTECH INC.

Chen J, Goddard A, Gurney AL, Pennica D, Wood WI, Yuan J;

WPI; 1999-229533/19.

N-PSDB; AAX52263.

New isolated human genes and polypeptides used in, e.g. treatment of  
 gastrointestinal ulceration

Claim 12; Fig 100; 320pp; English.

XX AA113344-403 represent secreted and transmembrane human proteins.  
 CC The cDNA sequences are obtained from cDNA libraries, prepared from  
 CC fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina.  
 CC The encoded polypeptides have specific uses based on their homology to  
 CC known polypeptides, e.g. PRO211 and PRO217 can be used for disorders  
 CC associated with the preservation and maintenance of gastrointestinal  
 CC mucosa and the repair of acute and chronic mucosal lesions  
 CC (e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal  
 CC ulceration and congenital microvillus atrophy), skin diseases associated  
 CC with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial  
 CC cancers such as lung squamous cell carcinoma of the vulva and gliomas),  
 CC potent effects on cell growth and development of diseases related to  
 CC growth or survival of nerve cells including Parkinson's disease,  
 CC Alzheimer's disease, ALS, neuropathies or cancer PRO265 can be used as  
 CC for fibromodulin, e.g. for reducing dermal scarring PRO264 can be used  
 CC as a target for anti-tumor drugs; PRO533 may be used in the treatment  
 CC of Usher Syndrome or Atrophia areata; PRO263 can be used as an  
 CC anti-thrombotic agent; PRO287 polypeptides and portions may have  
 CC therapeutic applications in wound healing and tissue repair; PRO317 can



CC cranial nerve disorders, spinal cord diseases, muscular dystrophy and  
CC other neuromuscular disorders, peripheral nervous system disorders,  
CC inherited, metabolic, endocrine and toxic myopathias, mental  
CC disorders including mood, anxiety and schizophrenic disorders, a cell  
CC proliferative disorder such as actinic keratosis, arteriosclerosis,  
CC thierosclerosis, burgitis, cirrhosis, hepatitis, mixed connective  
CC tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal  
CC haemoglobinuria, cancers of the adrenal gland, bladder, bone,  
CC bone marrow, brain, breast, cervix, and an autoimmune/inflammatory  
CC disorder such as acquired immunodeficiency syndrome (AIDS), Addison's  
CC disease, adult respiratory distress syndrome, allergies, ankylosing  
CC spondylitis, amyloidosis, anemia, asthma, Werner syndrome,  
CC complications of cancer, hemodialysis, and extracorporeal circulation,  
CC viral, bacterial, fungal parasitic, protozoal, and helminthic  
CC infections, and trauma. This protein was given the Incyte ID no.  
CC 2634931CD1.

XX Sequence 463 AA;

Query Match 15.98; Score 159; DB 21; Length 463;

Best Local Similarity 28.68; Pred. No. 9.8e-08;

Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;

OY 13 LDDDMREMTLHNGYRAFAFARNYKTSKMTWYDCTLEKAYKSAKC---SEEPSSE 68  
DB 28 LTDEERKLAVELHNLRYAQSPT--ASDMLHMRNDEELAAFAKAYARQCVMGHNREGR 85  
OY 69 EENVDFSAATLINIPLEAGNSWSEIFELRGKVNKNGKTSNIANN-----VWDSHDK 121  
DB 86 GEMTFALTDGMDVPL-AMEEWHE-----REHYNLSPAATCSPGOMCGHYTQVWAKTER 139  
OY 122 LGCAYVDCS-----GKTHV---VCOYGPFAKGDGKTIYEGAPCSRSDYAGVTCDDDW 173  
DB 140 IGGSHFEKLGVEETINIELVCAENPEPGNVKGRPYQEGTPCSOCP---SGYHC----- 192  
OY 174 QNLIC 178  
DB 193 KNSLIC 197

Search completed: July 15, 2003, 08:36:12  
Job time : 73 secs



Tue Jul 15 09:48:45 2003

us-09-937-555a-2.ra1

Page 1

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OM protein - protein search, using sw model

Run on: July 15, 2003, 08:32:08 ; Search time 26 Seconds  
(without alignments)  
204.823 Million cell updates/sec

Title: US-09-937-555a-2  
Perfect score: 997  
Sequence: 1 EGVSYLCCQREKIDDDMKEM.....DYAGACTCDDDMNLCTIGH 181

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents, AA.\*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep.\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	299	30.0	231	1 US-08-173-510B-86	Sequence 86, Appl
2	299	30.0	231	1 US-08-458-218-84	Sequence 84, Appl
3	299	30.0	231	2 US-08-450-497-86	Sequence 84, Appl
4	290.5	29.1	232	1 US-08-173-510B-84	Sequence 84, Appl
5	290.5	29.1	232	1 US-08-458-218-82	Sequence 82, Appl
6	290.5	29.1	232	2 US-08-450-497-83	Sequence 81, Appl
7	290	29.1	274	1 US-08-173-510B-83	Sequence 83, Appl
8	290	29.1	274	1 US-08-458-218-81	Sequence 83, Appl
9	290	29.1	274	2 US-08-450-497-81	Sequence 83, Appl
10	266	26.7	224	1 US-08-173-510B-87	Sequence 87, Appl
11	266	26.7	224	1 US-08-458-218-85	Sequence 87, Appl
12	266	26.7	224	2 US-08-450-497-85	Sequence 87, Appl
13	265.8	26.6	424	1 US-08-419-418-2	Sequence 2, Appl1
14	265	26.6	424	1 US-08-173-510B-85	Sequence 85, Appl
15	265	26.6	424	1 US-08-458-218-83	Sequence 85, Appl
16	265	26.6	424	1 US-08-450-497-83	Sequence 85, Appl
17	265	26.6	424	1 US-08-450-497-83	Sequence 85, Appl
18	265	26.6	424	1 US-08-450-497-83	Sequence 85, Appl
19	265	26.6	424	1 US-08-450-497-83	Sequence 85, Appl
20	265	26.6	424	1 US-08-450-497-83	Sequence 85, Appl
21	265	26.6	424	1 US-08-450-497-83	Sequence 85, Appl
22	265	26.6	424	1 US-08-450-497-83	Sequence 85, Appl
23	265	26.6	424	1 US-08-450-497-83	Sequence 85, Appl
24	265	26.6	424	1 US-08-450-497-83	Sequence 85, Appl
25	265	26.6	424	1 US-08-450-497-83	Sequence 85, Appl
26	265	26.6	424	1 US-08-450-497-83	Sequence 85, Appl
27	265	26.6	424	1 US-08-450-497-83	Sequence 85, Appl

28	151	15.1	270	3 US-09-199-887-1	Sequence 1, Appl1
29	144	14.4	146	1 US-08-173-510B-88	Sequence 88, Appl
30	144	14.4	146	1 US-08-458-218-86	Sequence 88, Appl
31	144	14.4	146	2 US-08-450-497-88	Sequence 88, Appl
32	141	14.1	205	5 US-08-450-944-5	Sequence 5, Appl1
33	141	14.1	205	5 PCT-US96-07709-5	Sequence 5, Appl1
34	141	14.1	221	1 US-08-450-944-2	Sequence 2, Appl1
35	141	14.1	221	5 PCT-US96-07709-2	Sequence 2, Appl1
36	127	12.7	138	2 US-07-857-224B-112	Sequence 112, Appl
37	122	12.2	266	2 US-08-773-368-4	Sequence 4, Appl1
38	122	12.2	266	2 US-09-199-887-4	Sequence 4, Appl1
39	121	12.1	219	2 US-08-173-368-3	Sequence 3, Appl1
40	121	12.1	219	2 US-09-199-887-3	Sequence 3, Appl1
41	115	11.5	137	2 US-07-857-224B-111	Sequence 111, Appl
42	112.5	11.3	204	1 US-08-614-935-5	Sequence 5, Appl1
43	112.5	11.3	204	3 US-09-130-287-5	Sequence 5, Appl1
44	110	11.0	205	1 US-08-614-935-4	Sequence 4, Appl1
45	110	11.0	205	3 US-09-130-287-4	Sequence 4, Appl1

#### ALIGNMENTS

RESULT 1  
US-08-173-510B-86  
Sequence 86, Application US/08173510B  
Patent No. 5747296  
GENERAL INFORMATION:  
APPLICANT: MATTHEW NOYF, ET AL.  
TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS  
NUMBER OF SEQUENCES: 104  
CORRESPONDING ADDRESS:  
ADDRESSER: Lyon 8 Lyon  
STREET: 633 West Pflin Street  
STREET: Suite 1700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 Diskette, 1.44 MB  
MEDIUM TYPE: Storage  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/173,510B  
FILING DATE: 23-DEC-1993  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: 08/151,064  
FILING DATE: 10-NOV-1993  
APPLICATION NUMBER: 08/060,433  
FILING DATE: 11-MAY-1993  
APPLICATION NUMBER: 07/996,972  
FILING DATE: 24-DEC-1992  
APPLICATION NUMBER: 07/881,721  
FILING DATE: 11-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 205/073  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 86:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 231 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
US-08-173-510B-86

Sequence 1, Appl1  
Sequence 88, Appl  
Sequence 88, Appl  
Sequence 88, Appl  
Sequence 5, Appl1  
Sequence 2, Appl1  
Sequence 112, Appl  
Sequence 4, Appl1  
Sequence 3, Appl1  
Sequence 3, Appl1  
Sequence 111, Appl  
Sequence 5, Appl1  
Sequence 4, Appl1  
Sequence 4, Appl1

Query Match 30.0%; Score 299; DB 1; Length 231;  
Best Local Similarity 35.2%; Pred. No. 4.2e-25;  
Matches 74; Conservative 20; Mismatches 58; Indels 58; Gaps 8;

QY 6 LCOQREK-----LDDHMEFTELHNGYRAAFARNY----- 36  
DB 16 ICSQNGTGFHFNDSMRKFLFEMHNGYRLALGHISITPEPSYDDDDYGYSEVLYAP 75  
QY 37 KTSKRTMYTDCITLBEKAYSAKESGSEPSSE-----BENDVPSAATLNIPLEA 86  
DB 76 SASKRTMYETDCBEKSAKYSASSCSOSSPEGYDENKTYILENSSNISSEARLAI----- 131  
QY 87 GNSWSEIFEL---RKYVKNKGTSTIANWVDSHDKLGCAVDDCSGK-----THVY 136  
DB 132 -LSMAEAFDLNKTGEGVLYRSLTISFNAILANDTREKFGCAVACPLKDTSATTHVY 190  
QY 137 CQYGPBANG--DGKTYIEGAPCSRCSDY 163  
DB 191 CHY-PRIEGEKEGKQIYKVTGTCGDCSEY 219

RESULT 2  
US-08-458-218-84  
; Sequence 84, Application US/08458218  
; Patent No. 5789178  
; GENERAL INFORMATION:  
; APPLICANT: MATTHEW MOYLE ET AL.  
; TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS  
; NUMBER OF SEQUENCES: 102  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/458,218  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/151,064  
; FILING DATE: 10-NOVEMBER-1993  
; APPLICATION NUMBER: 08/060,433  
; FILING DATE: 11-MAY-1993  
; APPLICATION NUMBER: 07/861,721  
; FILING DATE: 11-MAY-1992  
; APPLICATION NUMBER: 07/996,972  
; FILING DATE: 24-DEC-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BIGGS, SUZANNE L.  
; REGISTRATION NUMBER: 30,158  
; REFERENCE/DOCKET NUMBER: 203/226  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 84:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 231 AMINO ACIDS  
; TYPE: AMINO ACID  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PEPTIDE  
US-08-458-218-84

Query Match 30.0%; Score 299; DB 1; Length 231;

Best Local Similarity 35.2%; Pred. No. 4.2e-25;  
Matches 74; Conservative 20; Mismatches 58; Indels 58; Gaps 8;

QY 6 LCOQREK-----LDDHMEFTELHNGYRAAFARNY----- 36  
DB 16 ICSQNGTGFHFNDSMRKFLFEMHNGYRLALGHISITPEPSYDDDDYGYSEVLYAP 75  
QY 37 KTSKRTMYTDCITLBEKAYSAKESGSEPSSE-----BENDVPSAATLNIPLEA 86  
DB 76 SASKRTMYETDCBEKSAKYSASSCSOSSPEGYDENKTYILENSSNISSEARLAI----- 131  
QY 87 GNSWSEIFEL---RKYVKNKGTSTIANWVDSHDKLGCAVDDCSGK-----THVY 136  
DB 132 -LSMAEAFDLNKTGEGVLYRSLTISFNAILANDTREKFGCAVACPLKDTSATTHVY 190  
QY 137 CQYGPBANG--DGKTYIEGAPCSRCSDY 163  
DB 191 CHY-PRIEGEKEGKQIYKVTGTCGDCSEY 219

RESULT 3  
US-08-450-497-86  
; Sequence 86, Application US/08450497  
; Patent No. 5919900  
; GENERAL INFORMATION:  
; APPLICANT: MATTHEW MOYLE, ET AL.  
; TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS  
; NUMBER OF SEQUENCES: 104  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
; MEDIUM TYPE: storage  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/450,497  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/173,510  
; FILING DATE: 23-DEC-1993  
; APPLICATION NUMBER: 08/151,064  
; FILING DATE: 10-NOV-1993  
; APPLICATION NUMBER: 08/060,433  
; FILING DATE: 11-MAY-1993  
; APPLICATION NUMBER: 07/996,972  
; FILING DATE: 24-DEC-1992  
; APPLICATION NUMBER: 07/861,721  
; FILING DATE: 11-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BIGGS, SUZANNE L.  
; REGISTRATION NUMBER: 30,158  
; REFERENCE/DOCKET NUMBER: 205/073  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ ID NO: 86:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 231 AMINO ACIDS  
; TYPE: AMINO ACID  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PEPTIDE  
US-08-450-497-86

Query Match 30.0%; Score 299; DB 2; Length 231;

Best Local Similarity 35.2%; Pred. No. 4.2e-25;  
Matches 74; Conservative 20; Mismatches 58; Indels 58; Gaps 8;  
Db 6 LCOORER-----LDDMRKRETELHNGYRAAFARNY-----K 37  
16 ICSNGRCMGFNDSIRLKFLEHNGYRSLALGHVSTEESEEDYDLVLLYAR 96  
37 KTSKMTWYDCTLEEKAYSAKCSSEPSSE-----ENVDSATLNIPLEA 87  
76 SASKMTWYDCTLEEKAYSAKCSSEPSSE-----ENVDSATLNIPLEA 131  
87 GNSWSEIFEL-----RGVYNKNGKTSNANWYDSHDKLCAVYDCSGK-THVY 136  
132 LSNMATEAFDNLKTEGVLVYRSNLITISNPNLAMDTRKFCVAVKCPKIDTSATTIHV 190  
137 CGYGEPAKG---DGTIYESGAPCSRCSDY 163  
191 CHY-PKIEGEKRGKQIYKVGTPCGDCSEY 219

RESULT 4  
US-08-173-510B-84  
Sequence 84, Application US/08173510B  
Patent No. 5747296  
GENERAL INFORMATION:  
APPLICANT: MATTHEM MOYLE, ET AL.  
TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS  
NUMBER OF SEQUENCES: 104  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/173, 510B  
FILING DATE: 23-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/151,064  
FILING DATE: 10-NOV-1993  
APPLICATION NUMBER: 08/060,433  
FILING DATE: 11-MAY-1993  
APPLICATION NUMBER: 07/996,972  
FILING DATE: 24-DEC-1992  
APPLICATION NUMBER: 07/881,721  
FILING DATE: 11-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 205/073  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 84:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 232 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
US-08-173-510B-84

Query Match 29.1%; Score 290.5; DB 1; Length 232;  
Best Local Similarity 37.3%; Pred. No. 3.6e-24;  
Matches 75; Conservative 23; Mismatches 60; Indels 43; Gaps 7;

Db 1 EDDYSLCOQREK-----DDMRKRETELHNGYRAAFARNY-----K 37  
37 EHDPTCPQNGKMKKGFDDAIRLKLFLAMHNGYRSRLALGHVSTEESEEDYDLVLLYAR 96  
38 TSKMTWYDCTLEEKAYSAKCSSEPSSE-----ENVDSATLNIPLEA 87  
97 ASKMTWYDCTLEEKAYSAKCSSEPSSE-----ENVDSATLNIPLEA 151  
88 NSWSEIFEL-----RGVYNKNGKTSNANWYDSHDKLCAVYDCSGK-THVY 142  
152 LSNMATEAFDNLKTEGVLVYRSNLITISNPNLAMDTRKFCVAVKCPKIDTSATTIHV 211  
143 AKGDGKTIYERGAAPCSRCSDY 163  
212 SRKRNENPYTTGNRCGCGSDY 232

RESULT 5  
US-08-458-218-82  
Sequence 82, Application US/08458218  
Patent No. 5789178  
GENERAL INFORMATION:  
APPLICANT: MATTHEM MOYLE ET AL.  
TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS  
NUMBER OF SEQUENCES: 102  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/458, 218  
FILING DATE: 24-DEC-1992  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/151,064  
FILING DATE: 10-NOVEMBER-1993  
APPLICATION NUMBER: 08/060,433  
FILING DATE: 11-MAY-1993  
APPLICATION NUMBER: 07/996,972  
FILING DATE: 24-DEC-1992  
APPLICATION NUMBER: 07/881,721  
FILING DATE: 11-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 203/226  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 82:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 232 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
US-08-458-218-82

Query Match 29.1%; Score 290.5; DB 1; Length 232;  
Best Local Similarity 37.3%; Pred. No. 3.6e-24;  
Matches 75; Conservative 23; Mismatches 60; Indels 43; Gaps 7;

QY 1 EGDYSLCOQREKL-----DDMRMFTLHNGYRAAFARNY-----R 37  
DB 37 EHPPTCPONGEMERKGFDDAIRKFLAMHNGYRSRLAGHVSITERSEDDYLDLYLAPR 96  
QY 38 TSKRTMYVDTLEEKAYSAEKSEBPSSEB---ENV-----DVSAAATLNIPLAC 87  
DB 97 ASQMRKLKDCDEAKRSAYESAKKCOYTASWEKEDENI.QVIEDPKINHA-----LKAI 151  
QY 88 NSWMSIEFL-----RGVYKNGKTSNLIANNVMDSHDKLCAVVDSCGK-THVVCQGYPE 142  
DB 152 ISWATEAFNLKNTGEGVYRSILDISNFAANLAMPTRKREKVCACAVKCSPTTHVCHYPRK 211  
QY 143 AKGDGRTYEBGAPCSRCSDY 163  
DB 212 SRKRNPIYTTGNRCGCSY 232

RESULT 6  
US-08-450-497-84  
Sequence 84, Application US/08450497  
Patent No. 5919900  
GENERAL INFORMATION:  
APPLICANT: MATTHEW MOYLE, ET AL.  
TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS  
NUMBER OF SEQUENCES: 104  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,497  
FILING DATE: 23-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/173,510  
FILING DATE: 23-DEC-1993  
APPLICATION NUMBER: 08/151,064  
FILING DATE: 10-NOV-1993  
APPLICATION NUMBER: 08/060,433  
FILING DATE: 11-MAY-1993  
APPLICATION NUMBER: 07/996,972  
FILING DATE: 24-DEC-1992  
APPLICATION NUMBER: 07/881,721  
FILING DATE: 11-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 205/073  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 84:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 232 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
US-08-450-497-84

Query Match 29.1%; Score 290.5; DB 2; Length 232;  
Best Local Similarity 37.3%; Pred. No. 3.6e-24;  
Matches 75; Conservative 23; Mismatches 60; Indels 43; Gaps 7;

QY 1 EGDYSLCOQREKL-----DDMRMFTLHNGYRAAFARNY-----R 37  
DB 37 EHPPTCPONGEMERKGFDDAIRKFLAMHNGYRSRLAGHVSITERSEDDYLDLYLAPR 96  
QY 38 TSKRTMYVDTLEEKAYSAEKSEBPSSEB---ENV-----DVSAAATLNIPLAC 87  
DB 97 ASQMRKLKDCDEAKRSAYESAKKCOYTASWEKEDENI.QVIEDPKINHA-----LKAI 151  
QY 88 NSWMSIEFL-----RGVYKNGKTSNLIANNVMDSHDKLCAVVDSCGK-THVVCQGYPE 142  
DB 152 ISWATEAFNLKNTGEGVYRSILDISNFAANLAMPTRKREKVCACAVKCSPTTHVCHYPRK 211  
QY 143 AKGDGRTYEBGAPCSRCSDY 163  
DB 212 SRKRNPIYTTGNRCGCSY 232

RESULT 7  
US-08-173-510B-83  
Sequence 83, Application US/08173510B  
Patent No. 5747296  
GENERAL INFORMATION:  
APPLICANT: MATTHEW MOYLE, ET AL.  
TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS  
NUMBER OF SEQUENCES: 104  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/173,510B  
FILING DATE: 23-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/151,064  
FILING DATE: 10-NOV-1993  
APPLICATION NUMBER: 08/060,433  
FILING DATE: 11-MAY-1993  
APPLICATION NUMBER: 07/996,972  
FILING DATE: 24-DEC-1992  
APPLICATION NUMBER: 07/881,721  
FILING DATE: 11-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 205/073  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 83:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 274 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
US-08-173-510B-83

Query Match 29.1%; Score 290; DB 1; Length 274;  
Best Local Similarity 34.3%; Pred. No. 5.3e-24;  
Matches 69; Conservative 23; Mismatches 57; Indels 52; Gaps 7;

Tue Jul 15 09:48:45 2003

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Page 5

Db 35 ND\$IR\$Q\$F\$AM\$NG\$R\$K\$AL\$G\$H\$IT\$TE\$RS\$D\$DD\$D\$D\$F\$G\$LP\$D\$F\$P\$R\$A\$S\$K\$M\$R\$Y\$LE\$Y\$D\$E\$A 94

Qy 51 E\$K\$R\$Y\$A\$K\$E\$C\$E\$---P\$S\$E\$E\$N\$D\$V\$S\$A\$T\$U\$I\$---P\$L\$E\$G\$N\$S\$M\$S\$E\$F\$E\$L\$-----R 98

Db 95 E\$K\$A\$Y\$S\$A\$N\$C\$D\$S\$S\$P\$E\$G\$E\$Y\$D\$N\$K\$Y\$E\$N\$N\$-N\$I\$S\$A\$L\$K\$M\$I\$S\$M\$A\$K\$E\$P\$N\$I\$N\$K\$E\$E 155

Qy 99 G\$K\$Y\$N\$N\$G\$T\$S\$I\$N\$M\$W\$D\$H\$K\$I\$G\$A\$V\$V\$C\$-----S\$G\$T\$-----H\$Y\$C\$O\$Y\$P\$E 142

Db 154 G\$Y\$I\$R\$S\$M\$H\$D\$I\$S\$F\$A\$N\$L\$M\$D\$R\$E\$F\$G\$A\$V\$N\$C\$P\$A\$G\$E\$ID\$D\$E\$T\$H\$D\$E\$T\$A\$T\$T\$H\$V\$C\$H\$P\$R\$I 213

Qy 143 A\$K\$D\$G\$K\$T\$T\$E\$B\$G\$A\$P\$C\$S\$K\$S\$Y 163

Db 214 N\$K\$T\$E\$G\$P\$I\$K\$V\$G\$T\$P\$D\$D\$C\$S\$E\$Y 234

```

RESULT 8
US-08-458-218-81
: Sequence 81, Application US/08458218
: Patent No. 5789178
: GENERAL INFORMATION:
: APPLICANT: MATTHEW MOYLE ET AL.
: TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS
: NUMBER OF SEQUENCES: 102
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Lyon & Lyon
: STREET: 633 West Fifth Street
: STREET: Suite 4700
: CITY: Los Angeles
: STATE: California
: COUNTRY: U.S.A.
: ZIP: 90071
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5" Diskette, 1.44 MB
: MEDIUM TYPE: Storage
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: IBM P.C. DOS 5.0
: SOFTWARE: Word Perfect 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/458,218
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/151,064
: FILING DATE: 10-NOVEMBER-1993
: APPLICATION NUMBER: 08/060,433
: FILING DATE: 11-MAY-1993
: APPLICATION NUMBER: 07/881,721
: FILING DATE: 11-MAY-1992
: APPLICATION NUMBER: 07/996,972
: FILING DATE: 24-DEC-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: BIGGS, SZYMANNE L.
: REGISTRATION NUMBER: 30,158
: REFERENCE/DOCKET NUMBER: 203/226
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (213) 489-1600
: TELEFAX: (213) 955-0440
: TELEX: 67-3510
: INFORMATION FOR SEO ID NO: 81:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 274 AMINO ACIDS
: TYPE: AMINO ACIDS
: TOPOLOGY: LINEAR
: MOLECULE TYPE: PEPTIDE
:
: US-08-458-218-81

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[illegible]

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OY      14 DDDREMTTELANGYRAAARANY-----KTKMKNMYDCTL 50
db      35 NSDIRGLTGLAAHNSKRLAHISITSEESDDDDDDGFLPFAAPASAKMYLEYCCCA 94

US-08-450-497-83
Sequence 83, Application US/08450497
Patent No. 5919900
GENERAL INFORMATION:
APPLICANT: MATTHEW MOYLE, ET AL.
TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDION TYPE: 3.5" Diskette, 1.44 MB
MEDION TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,497
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/173,510
FILING DATE: 23-DEC-1993
APPLICATION NUMBER: 08/151,064
FILING DATE: 10-NOV-1993
APPLICATION NUMBER: 08/060,433
FILING DATE: 11-MAY-1993
APPLICATION NUMBER: 07/896,972
FILING DATE: 24-DEC-1992
APPLICATION NUMBER: 07/681,721
FILING DATE: 11-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SOZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 205/073
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1500
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ. ID NO.: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 274 AMINO ACIDS
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE
US-08-450-497-83
Query Match 29.18; Score 290; DB 2; Length 274;
Best Local Similarity 34.33; Pred. No. 5.3e-24;
Matches 69; Conservative 23; Mismatches 57; Indels 52; Gaps 7.

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Page 7

Db 91 AEA\$A\$M\$R\$R\$C\$O\$S\$S\$S\$P\$E\$G\$E\$D\$E\$N\$T\$Y\$I\$E\$N\$S\$N\$-N\$I\$E\$A\$L\$A\$L\$M\$I\$M\$A\$K\$E\$F\$N\$I\$N\$K\$T\$E\$G\$E 149

Qy 99 G\$K\$Y\$N\$N\$G\$K\$T\$S\$N\$A\$M\$W\$D\$S\$H\$D\$K\$L\$C\$C\$A\$Y\$V\$D\$C\$-----S\$K\$T\$----H\$Y\$C\$O\$G\$P\$E 142

Db 150 G\$V\$I\$R\$S\$N\$H\$D\$I\$S\$F\$N\$F\$N\$M\$L\$M\$D\$R\$E\$F\$C\$A\$V\$N\$C\$P\$L\$G\$E\$I\$D\$G\$T\$T\$H\$D\$E\$Y\$A\$V\$T\$H\$V\$C\$H\$Y\$P\$K\$M 209

Qy 143 A\$K\$G\$D\$G\$T\$T\$E\$G\$A\$P\$C 157

Db 210 N\$K\$T\$E\$G\$P\$I\$R\$K\$Y\$G\$P\$C 224

## RESULT 13

Sequence 2, Application US/08419414

; PATENT NO. 375378/  
; GENERAL INFORMATION:

```

;
;
APPLICANT: HAWDOH, JOHN M.
APPLICANT: HOTEZ, PETER J.
;

```

APPLICANT: Jones, Brian F.  
TITLE OF INVENTION: Hookworm Vaccine

NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Patrea L. Pabst  
CREDIT: 3600 0-0 141-444 0-4-4

STREET: 1201 West Peachtree Street

STATE: Georgia

COUNTRY: USA  
ZIP: 30309-3450

COMPUTER READABLE FORM:  
MEDIUM TYPE: E10000 414k

COMPUTER: IBM PC compatible

SOFTWARE: Patentin Release #1.0, V

APPLICANT AFFILIATION DATA:  
CURRENT AFFILIATION NUMBER: US/08/419,414

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:  
NAME: Babst Patricia L.

REGISTRATION NUMBER: 31,284

TELECOMMUNICATION INFORMATION:

TELEPHONE: (404) 873-8795  
TELEFAX: (404) 873-8795

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; INFORMATION FOR SEQ ID NO: 2:
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; SEQUENCE CHARACTERISTICS:

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LENGTH: 424 amino acids  
TYPE: amino acid

STRANDEDNESS:  
TOTAL: 14

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      MOLECULE TYPE:  protein

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ANTI-SENSE: NO

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; ORIGINAL SOURCE:
; ORGANISM: Ancylostoma caninum

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DEVELOPMENTAL STAGE: LARVA  
PS-08-419-414-2

Quarter Match 25 50 100 250

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Model 99	32.58; Pred. No	
Model 100	32.58; Pred. No	

11/2 3476438000 1/2 3476438000  
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by / CQ9REKDDDMKREMETELHNGYKAAR

Db 227 CPSNTGMTDSVRDTFLSVHNEFRSSVAR

QY 57 SAEKSEEPSSEEE---NVDVFSATL

Db . 287 HGNKCVYQHSHGGEPRPGLGENITYKTSVL

QY 100 KVNKNG-KTSNIANMWDSDHDKLGCAV

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Db 347 ALNRPMGJGHTYQAMDTYKLGAVNFCNFTFGVQYGPGRNMGVITMGPQCS 406  
QY 159 RCDYAGACATC 169  
Db 407 GCS---PGATC 414

## RESULT 14

US-08-173-510B-85  
; Sequence 85: Application US/08173510B  
; Patent No. 5747266  
; GENERAL INFORMATION:  
; APPLICANT: MATTHEW MOYLE, ET AL.  
; TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS  
; NUMBER OF SEQUENCES: 104  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; OPERATING SYSTEM: IBM P.C. DOS 5.0  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/173, 510B  
; FILING DATE: 23-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/151,064  
; FILING DATE: 10-NOV-1993  
; APPLICATION NUMBER: 08/060,433  
; FILING DATE: 11-MAY-1993  
; APPLICATION NUMBER: 07/996,972  
; FILING DATE: 24-DEC-1992  
; APPLICATION NUMBER: 07/881,721  
; FILING DATE: 11-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BIGGS, SUZANNE L.  
; REGISTRATION NUMBER: 30,158  
; REFERENCE/DOCKET NUMBER: 205/073  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ. ID NO: 85:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 208 AMINO ACIDS  
; TYPE: AMINO ACID  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PEPTIDE  
US-08-173-510B-85

Query Match 25.6%; Score 255; DB 1; Length 208;  
Best Local Similarity 36.5%; Pred. No. 2,6e-20;  
Matches 65; Conservative 18; Mismatches 55; Indels 40; Gaps 8;  
QY 14 DDDKREMFELHNGYRAAFARNY--KTSKRTIWDCTLEKAYKSAKC--SEPPSSE 68  
Db 3 DDD-----YEGFLPDPFAPRASKRYLEYDCEAEKSAVYASNSNSISPPGCGY 51  
QY 69 EENDVFSATLNI--PLEAGNSWSEIFEL---RGKRVYKNGKTSNANVWDSHDK 121  
Db 52 DENKTIENSNN-NISBALAKAMISMAKFAFNLNKKTGEGLYRSMNLTISNPNANLMDTREQ 110  
QY 122 LGCAVVDGS-GK-----THVVCYGPENKGDGKTIYEGAPGCSRCSY 163  
Db 111 FGCAVAVNCPGKRDALITDDEENYATAIHVYCHYPRINKTEGQPIYKVGTPCDDCSEY 168

## RESULT 15

US-08-458-218-83  
; Sequence 83: Application US/08458218  
; Patent No. 5785178  
; GENERAL INFORMATION:  
; APPLICANT: MATTHEW MOYLE ET AL.  
; TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS  
; NUMBER OF SEQUENCES: 102  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Lyon & Lyon  
; STREET: 633 West Fifth Street  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
; MEDIUM TYPE: storage  
; OPERATING SYSTEM: IBM Compatible  
; SOFTWARE: Word Perfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/458, 218  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/151,064  
; FILING DATE: 10-NOVEMBER-1993  
; APPLICATION NUMBER: 08/060,433  
; FILING DATE: 11-MAY-1993  
; APPLICATION NUMBER: 07/881,721  
; FILING DATE: 11-MAY-1992  
; APPLICATION NUMBER: 07/996,972  
; FILING DATE: 24-DEC-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BIGGS, SUZANNE L.  
; REGISTRATION NUMBER: 30,158  
; REFERENCE/DOCKET NUMBER: 203/226  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (213) 489-1600  
; TELEFAX: (213) 955-0440  
; TELEX: 67-3510  
; INFORMATION FOR SEQ. ID NO: 83:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 208 AMINO ACIDS  
; TYPE: AMINO ACID  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PEPTIDE  
US-08-458-218-83

Query Match 25.6%; Score 255; DB 1; Length 208;  
Best Local Similarity 36.5%; Pred. No. 2,6e-20;  
Matches 65; Conservative 18; Mismatches 55; Indels 40; Gaps 8;  
QY 14 DDDKREMFELHNGYRAAFARNY--KTSKRTIWDCTLEKAYKSAKC--SEPPSSE 68  
Db 3 DDD-----YEGFLPDPFAPRASKRYLEYDCEAEKSAVYASNSNSISPPGCGY 51  
QY 69 EENDVFSATLNI--PLEAGNSWSEIFEL---RGKRVYKNGKTSNANVWDSHDK 121  
Db 52 DENKTIENSNN-NISBALAKAMISMAKFAFNLNKKTGEGLYRSMNLTISNPNANLMDTREQ 110  
QY 122 LGCAVVDGS-GK-----THVVCYGPENKGDGKTIYEGAPGCSRCSY 163  
Db 111 FGCAVAVNCPGKRDALITDDEENYATAIHVYCHYPRINKTEGQPIYKVGTPCDDCSEY 168  
RESULT 16  
US-08-450-497-85  
; Sequence 85: Application US/08450497  
; Patent No. 5919300



```

GENERAL INFORMATION:
APPLICANT: MATTHEW MOYLE, ET AL.
TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS
NUMBER OF SEQUENCES: 104
CORRESPONDENCE ADDRESS:
ADDRESS: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: Suite 4700
COUNTRY: California
ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,497
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/173,510
FILING DATE: 23-DEC-1993
APPLICATION NUMBER: 08/151,064
FILING DATE: 10-NOV-1993
APPLICATION NUMBER: 08/060,433
FILING DATE: 11-MAY-1993
APPLICATION NUMBER: 07/996,972
FILING DATE: 24-DEC-1992
APPLICATION NUMBER: 07/881,721
FILING DATE: 11-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 205/073
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 208 AMINO ACIDS
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE
US-08-450-497-85

Query Match 25.68; Score 255; DB 2; Length 208;
Best Local Similarity 36.58; Pred. No. 2.6e-20;
Matches 65; Conservative 18; Mismatches 55; Indels 40; Gaps 8;

QY 14 DDDAREFTELHNGYAAAFARNY--KTSKRTVYTCGLEEKAYSAKRC---SEEPSSE 68
DB 3 DDD-----YKGLPDPAPRAKSKMTLETCDAEKSAIYASNSCSNISPEPGY 51
QY 69 EENDVYSAAATLNI---PLEAGNSWSEIFEL---RGKRYNKGKTSNINANNYWDSDHK 121
DB 52 DENKTIENSN-NISPAALKAMISWAKDAFNLNKGTGEGVLYRNSLTJTSNFRANLMDTRK 110

QY 122 LGCAVYDCS-GK-----THVYCOYGEPAAGDGKTYIEGAPCSRCSY 163
DB 111 FGCNAVMPJGKPDALTITDEENATATAHVACHYPRINTSGOPTKYKGTGPPCDSCEY 168

RESULT 17
US-07-930-686-10
; Sequence 10, Application US/07930686
; Patent No. 5525508
; GENERAL INFORMATION:
; APPLICANT: Sharp, Phillip J
; APPLICANT: Wagland, Barry M
; APPLICANT: Cobon, Gary S

```

```

TITLE OF INVENTION: Nematode Vaccine
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESS: Foley and Lardner
STREET: Suite 500, 1800 Diagonal Road
CITY: Alexandria
STATE: Virginia
COUNTRY: United States of America
ZIP: 22313-0299

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/930,686
FILING DATE: 19921006
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PK4486
FILING DATE: 06-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU92/00040
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A
REGISTRATION NUMBER: 29,768
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEFAX: (703) 683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 454 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-930-686-10

Query Match 20.68; Score 205; DB 1; Length 454;
Best Local Similarity 28.58; Pred. No. 2.7e-14;
Matches 55; Conservative 36; Mismatches 74; Indels 28; Gaps 8;

QY 13 LDDAREFTELHNGYAAAFARNY-----KTSKRTVYTCGLEEKAYSAKCS 62
DB 262 MIDEARKRFVDKHEHYSLIAKGAQKRGQFAPKARBAWYKYNICDDEANAMSKTCT 321
QY 63 EEPSSE-----EENDVYSAAATLNI---PLEAGNSWSEIFEL---RGKRYNKGK-- 108
DB 322 FGLNTRALUKMGWNNMMSKANKKTEAAAEVAAWFGDLKTYGVPENNVFTYNYTTLL 381
QY 109 SINANNYWDSDHKLGCAVYDC-SGKTHVYCOYGEPAAGDGKTYIEGAPCSRCSYGA-G 166
DB 382 SKYSQAWSSDRIGCVYPCWSSWTVVCCERPNCGDLREALITDVGDPCTKADDCOCPE 441

QY 167 VYCDDDMONLICI 179
DB 442 CYCSRD--EGLCV 452

RESULT 18
US-08-460-998-10
; Sequence 10, Application US/08460998
; Patent No. 5942413
; GENERAL INFORMATION:
; APPLICANT: Sharp, Phillip J
; APPLICANT: Wagland, Barry M
; APPLICANT: Cobon, Gary S
; TITLE OF INVENTION: Nematode Vaccine
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley and Lardner
; STREET: suite 500, 3000 K Street, NW

```

CITY: Washington  
STATE: DC  
COUNTRY: United States of America  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: 05/08/460, 998  
FILING DATE: 05-JUN-1995  
APPLICATION NUMBER: 05/07/930, 666  
FILING DATE: 06-OCT-1992  
APPLICATION NUMBER: AU PK4486  
FILING DATE: 06-FEB-1991  
APPLICATION NUMBER: PCT/AU92/00040  
FILING DATE: 06-FEB-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Bent, Stephen A  
REGISTRATION NUMBER: 29,768  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 454 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-460-998-10

Query Match 20.6%; Score 205; DB 2; Length 454;  
Best Local Similarity 28.5%; Pred. No. 2,7e-14;  
Matches 55; Conservative 36; Mismatches 74; Indels 28; Gaps 8;

OY 13 LDDDNEMETELHNGYRAAFARNY-----KTSKRTWYVCT 49  
DB 262 MTEAKRFVDRKHNHRSLSLAKGAKGPGAPFAAARMKVVYDGDVANAEMWSTCT 321  
OY 63 EEDSSEE-----ENVDFSAATLN---IPLEGNSWSEIFEL---RGKYNNKNGKT-- 108  
DB 322 FGLNTAAMLRKGNMNMMSKANNTTEAAAEVAAMFGDLQKYGVPENNVFTWVYTTL 381  
OY 109 SNIANNVMDSHDKLGCAYVDC-SGKTHVYCOYGPAPKDGKTIYEGAGCSCSDYGA-G 166  
DB 382 SKYSQAMQSDRIGCYVPCNSMTVYVCENPGDLPGLPGLATIDVGDPCITADQCQCPG 441  
OY 167 VTGDDDMQWLICI 179  
DB 442 CTCGRD--EGLCV 452

RESULT 19  
US-08-173-5108-89  
Sequence 89; Application US/081735108  
Patent No. 5747296  
GENERAL INFORMATION:  
APPLICANT: MATTHEW MOYLE ET AL.  
TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS  
NUMBER OF SEQUENCES: 104  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
MEDIUM TYPE: storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 08/08/173, 5108  
FILING DATE: 23-DEC-1993  
APPLICATION NUMBER: 08/151, 064  
FILING DATE: 10-NOV-1993  
APPLICATION NUMBER: 08/060, 433  
FILING DATE: 11-MAY-1993  
APPLICATION NUMBER: 07/996, 972  
FILING DATE: 24-DEC-1992  
APPLICATION NUMBER: 07/881, 721  
FILING DATE: 11-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 205/073  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 89:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 189 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
US-08-173-5108-89

Query Match 20.1%; Score 200; DB 1; Length 189;  
Best Local Similarity 32.9%; Pred. No. 2,7e-14;  
Matches 50; Conservative 16; Mismatches 46; Indels 40; Gaps 6;

OY 15 DDHKEMETELHNGYRAAFARNY-----KTSKRTWYVCT 49  
DB 40 DSIRLFLAMHNGYSNLALGHIGIKESIGDDYDDVYFYSVAPMAKRYLEYDCD 99  
OY 50 LEEAVAKSEKSEE---PSSEENVDF-SAAVLNIPLEGN---SWMSEIFEL--- 97  
DB 100 SENSAYMSNSGSDSSPPEGYDENKYLLENSNIN---EAARLAIIISGKRAFLNLTG 156  
OY 98 RGKYNNKNGKTSTINANNVMDSHDKLGCAYVDC 129  
DB 157 EGYLVISNLTISFANLANMDTRREKFGCAVVKC 188

RESULT 20  
US-08-458-218-87  
Sequence 87; Application US/08458218  
Patent No. 5780178  
GENERAL INFORMATION:  
APPLICANT: MATTHEW MOYLE ET AL.  
TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS  
NUMBER OF SEQUENCES: 102  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
MEDIUM TYPE: storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1



FILING DATE: 06-FEB-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Bent, Stephen A.  
REGISTRATION NUMBER: 29,768  
TELEPHONE: (703) 836-9300  
TELEFAX: (703) 683-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 440 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-930-686-12

Query Match 19.88; Score 197.5; DB 1; Length 440;  
Best Local Similarity 27.78; Pred. No. 1.8e-13;  
Matches 57; Conservative 35; Mismatches 77; Indels 37; Gaps 11;

DB 6 LCOQREK-LDDMRKMTLHNGYRAAFARNY-----KTSKRTMYDCTLEKA 54  
DB 238 MCPENNNGMTDEAROMFVDKHNKSLIKGLAHNNIGFAPFAAAMKRVSYNCEIEANR 297  
QY 55 YKSAKCESEPSSEEN---VDVSAAT-LNIPLEGNS--WME-----IFE 96  
DB 298 VEMAKDCTLGYNVAQNONGYVHSLPHINKTVAAESVEAMFELQTYGAPQDNVFS 357  
QY 97 LRGKYNNKGTSTIANMWDSDKLGCAVDCSG--KTHVQCQYPEAKGDKTYIEEG 154  
DB 358 M--EVENON-VIQEYALQAMQSSNOIGCIFSCWGAFTVACEYINPGNFTIGELITMG 414  
QY 155 APCSRCS-D-YGAGVTCDDDMONLICT 179  
DB 415 DPCSTDEDCQACGVCCKD--EALCI 438

RESULT 23  
US-08-460-998-12  
Sequence 12, Application US/08460998  
Patent No. 5942413  
GENERAL INFORMATION:  
APPLICANT: Sharp, Phillip J  
APPLICANT: Magland, Barry M  
APPLICANT: Cobon, Gary S  
TITLE OF INVENTION: Nematode Vaccine  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley and Lardner  
STREET: suite 500, 3000 K Street, NW  
CITY: Washington  
STATE: DC  
COUNTRY: United States of America  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/460,998  
FILING DATE: 05-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/930,686  
FILING DATE: 06-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: AU PK4486  
FILING DATE: 06-FEB-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/AU92/00040  
FILING DATE: 06-FEB-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Bent, Stephen A

REGISTRATION NUMBER: 29,768  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 440 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-460-998-12

Query Match 19.88; Score 197.5; DB 2; Length 440;  
Best Local Similarity 27.78; Pred. No. 1.8e-13;  
Matches 57; Conservative 35; Mismatches 77; Indels 37; Gaps 11;

QY 6 LCOQREK-LDDMRKMTLHNGYRAAFARNY-----KTSKRTMYDCTLEKA 54  
DB 238 MCPENNNGMTDEAROMFVDKHNKSLIKGLAHNNIGFAPFAAAMKRVSYNCEIEANR 297  
QY 55 YKSAKCESEPSSEEN---VDVSAAT-LNIPLEGNS--WME-----IFE 96  
DB 298 VEMAKDCTLGYNVAQNONGYVHSLPHINKTVAAESVEAMFELQTYGAPQDNVFS 357  
QY 97 LRGKYNNKGTSTIANMWDSDKLGCAVDCSG--KTHVQCQYPEAKGDKTYIEEG 154  
DB 358 M--EVENON-VIQEYALQAMQSSNOIGCIFSCWGAFTVACEYINPGNFTIGELITMG 414  
QY 155 APCSRCS-D-YGAGVTCDDDMONLICT 179  
DB 415 DPCSTDEDCQACGVCCKD--EALCI 438

RESULT 24  
PCT-US96-07709-33  
Sequence 33, Application PC/TUS9607709  
GENERAL INFORMATION:  
APPLICANT: Timp, Cynthia A.  
APPLICANT: Wisniewski, Nancy  
TITLE OF INVENTION: PARASITIC HELMINTH VENOM ALLERGEN  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheridan Ross & McIntosh  
STREET: 1700 Lincoln St., Suite 3500  
CITY: Denver  
STATE: Colorado  
COUNTRY: U.S.A.  
ZIP: 80203  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/07709  
FILING DATE: 23-MAY-1996  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Connell, Gary J.  
REGISTRATION NUMBER: 32,020  
REFERENCE/DOCKET NUMBER: 2618-30-PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 863-9700  
TELEFAX: (303) 863-0223  
INFORMATION FOR SEQ ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 204 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US96-07709-33

Query Match 15.5%; Score 155; DB 5; Length 204;  
Best Local Similarity 26.4%; Pred. No. 2.8e-09;  
Matches 48; Conservative 24; Mismatches 68; Indels 42; Gaps 9;

QY 9 OREKLDMDREMFTELHNGYRAAFARNY--KTSKMTVYDCTLEEKAYSAKCC--SEE 64  
DB 12 ERKIVQNNKRYSDLNGKLKNNRGTYMPRGKMLTELMDCKLESSAQRMANQCIFFGHS 71  
QY 65 PSSEENV--DVF-----SAATLNIPLDAGNSMSEIFELRGVYNNKNGKTS 109  
DB 72 PROGREGVGENYAYVSSVSEGLKKTAGT----DAGKSMWSEL---PLYENPNN 122  
QY 110 -----NIANNWMSHDKLGCAV-VDCSG--KTHVCOYGEPAKGDGKTIYEBGA 155  
DB 123 MTKVAGGVHLFTOMAMGKTYKICGVAATCCDGRLLIVICHYSPGGMVGEVIYORGN 182  
QY 156 PC 157  
DB 183 PC 184

RESULT 25  
PCT-US96-07709-30  
; Sequence 30, Application PC/TUS9607709  
; GENERAL INFORMATION:  
; APPLICANT: Tripp, Cynthia A.  
; TITLE OF INVENTION: PARASITIC HELMINTH VENOM ALLERGEN  
; NUMBER OF INVENTIONS: PARASITIC 5-LIKE GENES AND PROTEINS  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sheridan Ross & McIntosh  
; STREET: 1700 Lincoln St., Suite 3500  
; CITY: Denver  
; STATE: Colorado  
; COUNTRY: U.S.A.  
; ZIP: 80203  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE: 23-MAY-1996  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Connell, Gary J.  
; REGISTRATION NUMBER: 32,020  
; REFERENCE/DOCKET NUMBER: 2618-30-PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (303) 863-9700  
; TELEFAX: (303) 863-0223  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 220 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; PCT-US96-07709-30

Query Match 15.5%; Score 155; DB 5; Length 220;  
Best Local Similarity 26.4%; Pred. No. 3.2e-09;  
Matches 48; Conservative 24; Mismatches 68; Indels 42; Gaps 9;

QY 9 OREKLDMDREMFTELHNGYRAAFARNY--KTSKMTVYDCTLEEKAYSAKCC--SEE 64  
DB 28 ERKIVQNNKRYSDLNGKLKNNRGTYMPRGKMLTELMDCKLESSAQRMANQCIFFGHS 87  
QY 65 PSSEENV--DVF-----SAATLNIPLDAGNSMSEIFELRGVYNNKNGKTS 109  
DB 88 PROGREGVGENYAYVSSVSEGLKKTAGT----DAGKSMWSEL---PLYENPNN 138

QY 110 -----NIANNWMSHDKLGCAV-VDCSG--KTHVCOYGEPAKGDGKTIYEBGA 155  
DB 139 MTKVAGGVHLFTOMAMGKTYKICGVAATCCDGRLLIVICHYSPGGMVGEVIYORGN 198  
QY 156 PC 157  
DB 199 PC 200

RESULT 26  
PCT-US96-07709-25  
; Sequence 25, Application PC/TUS9607709  
; GENERAL INFORMATION:  
; APPLICANT: Tripp, Cynthia A.  
; TITLE OF INVENTION: PARASITIC HELMINTH VENOM ALLERGEN  
; NUMBER OF INVENTIONS: PARASITIC 5-LIKE GENES AND PROTEINS  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sheridan Ross & McIntosh  
; STREET: 1700 Lincoln St., Suite 3500  
; CITY: Denver  
; STATE: Colorado  
; COUNTRY: U.S.A.  
; ZIP: 80203  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE: 23-MAY-1996  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Connell, Gary J.  
; REGISTRATION NUMBER: 32,020  
; REFERENCE/DOCKET NUMBER: 2618-30-PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (303) 863-9700  
; TELEFAX: (303) 863-0223  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 248 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; PCT-US96-07709-25

Query Match 15.5%; Score 155; DB 5; Length 248;  
Best Local Similarity 26.4%; Pred. No. 3.8e-09;  
Matches 48; Conservative 24; Mismatches 68; Indels 42; Gaps 9;

QY 9 OREKLDMDREMFTELHNGYRAAFARNY--KTSKMTVYDCTLEEKAYSAKCC--SEE 64  
DB 56 ERKIVQNNKRYSDLNGKLKNNRGTYMPRGKMLTELMDCKLESSAQRMANQCIFFGHS 115  
QY 65 PSSEENV--DVF-----SAATLNIPLDAGNSMSEIFELRGVYNNKNGKTS 109  
DB 116 PROGREGVGENYAYVSSVSEGLKKTAGT----DAGKSMWSEL---PLYENPNN 166  
QY 110 -----NIANNWMSHDKLGCAV-VDCSG--KTHVCOYGEPAKGDGKTIYEBGA 155  
DB 167 MTKVAGGVHLFTOMAMGKTYKICGVAATCCDGRLLIVICHYSPGGMVGEVIYORGN 226  
QY 156 PC 157  
DB 227 PC 228

RESULT 27  
US-08-773-368-1

```
Sequence 1, Application US/08773368
Patent No. 5856130
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
TITLE OF INVENTION: NOVEL HUMAN PATHOGENESIS-RELATED
NUMBER OF SEQUENCES: 6
ADDRESS: Inocyte Pharmaceuticals, Inc.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/773,368
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy RJ
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PE-0186 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 270 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: 1599164
US-08-773-368-1

Query Match
Best Local Similarity 28.1%; Score 151; DB 2; Length 270;
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 10;

OY 13 LDDMRNEMTELHNGYRAAFARNYKTSKRTWYDCTLE--EKAYSAEKC--SEEPSSE 68
DB 28 LTDEKRLMVELHNLHYRAOVSP--ASDMLHRMDEELAAFAKAYARQXKXGHNKRGRR 85
OY 69 EENVDFSAATINIPLEAGNSMSEIFELRGKYNNKNGKTSNIAM-----VWDSHX 121
DB 86 GENLFAITDEGMDVPL-AMEEMHNE-----REHYNLSAATCSPGQCGHYTVWAKTER 139
OY 122 LGCAYVDCS-----GKTHV---VCOYGPFAKGDGKTYEBSGPCSCSYGAGVTCDDW 173
DB 140 ICGSHCEKLGVEETNIELVCONTEPRGNVKKRPQESTPCSCP--SGYHC----- 192
OY 174 ONLJC 178
DB 193 KNSLC 197

RESULT 28
US-09-199-887-1
Sequence 1, Application US/09199887
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
ADDRESS: Inocyte Pharmaceuticals, Inc.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/199,887
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy RJ
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PE-0186 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 270 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: 1599164
US-09-199-887-1

Query Match
Best Local Similarity 28.6%; Score 151; DB 3; Length 270;
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 10;

OY 13 LDDMRNEMTELHNGYRAAFARNYKTSKRTWYDCTLE--EKAYSAEKC--SEEPSSE 68
DB 28 LTDEKRLMVELHNLHYRAOVSP--ASDMLHRMDEELAAFAKAYARQXKXGHNKRGRR 85
OY 69 EENVDFSAATINIPLEAGNSMSEIFELRGKYNNKNGKTSNIAM-----VWDSHX 121
DB 86 GENLFAITDEGMDVPL-AMEEMHNE-----REHYNLSAATCSPGQCGHYTVWAKTER 139
OY 122 LGCAYVDCS-----GKTHV---VCOYGPFAKGDGKTYEBSGPCSCSYGAGVTCDDW 173
DB 140 ICGSHCEKLGVEETNIELVCONTEPRGNVKKRPQESTPCSCP--SGYHC----- 192
OY 174 ONLJC 178
DB 193 KNSLC 197

RESULT 29
US-08-173-510B-88
Sequence 88, Application US/08173510B
GENERAL INFORMATION:
APPLICANT: MATTHEW MOYLE, ET AL.
TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS
NUMBER OF SEQUENCES: 104
ADDRESS: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,510B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy RJ
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PE-0186 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 270 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: 1599164
US-08-173-510B-88
```

```
Sequence 1, Application US/08773368
Patent No. 5856130
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
TITLE OF INVENTION: NOVEL HUMAN PATHOGENESIS-RELATED
NUMBER OF SEQUENCES: 6
ADDRESS: Inocyte Pharmaceuticals, Inc.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/773,368
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy RJ
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PE-0186 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 270 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: 1599164
US-08-773-368-1

Query Match
Best Local Similarity 28.6%; Score 151; DB 3; Length 270;
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 10;

OY 13 LDDMRNEMTELHNGYRAAFARNYKTSKRTWYDCTLE--EKAYSAEKC--SEEPSSE 68
DB 28 LTDEKRLMVELHNLHYRAOVSP--ASDMLHRMDEELAAFAKAYARQXKXGHNKRGRR 85
OY 69 EENVDFSAATINIPLEAGNSMSEIFELRGKYNNKNGKTSNIAM-----VWDSHX 121
DB 86 GENLFAITDEGMDVPL-AMEEMHNE-----REHYNLSAATCSPGQCGHYTVWAKTER 139
OY 122 LGCAYVDCS-----GKTHV---VCOYGPFAKGDGKTYEBSGPCSCSYGAGVTCDDW 173
DB 140 ICGSHCEKLGVEETNIELVCONTEPRGNVKKRPQESTPCSCP--SGYHC----- 192
OY 174 ONLJC 178
DB 193 KNSLC 197

RESULT 29
US-08-173-510B-88
Sequence 88, Application US/08173510B
GENERAL INFORMATION:
APPLICANT: MATTHEW MOYLE, ET AL.
TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS
NUMBER OF SEQUENCES: 104
ADDRESS: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,510B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy RJ
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PE-0186 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 270 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: 1599164
US-08-173-510B-88
```

CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 Diskette, 1.44 MB  
MEDIUM TYPE: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/173,510B  
FILING DATE: 23-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/151,064  
FILING DATE: 10-NOV-1993  
APPLICATION NUMBER: 08/060,433  
FILING DATE: 11-MAY-1993  
APPLICATION NUMBER: 07/996,972  
FILING DATE: 24-DEC-1992  
APPLICATION NUMBER: 07/881,721  
FILING DATE: 11-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 205/073  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 88:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 146 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
US-08-173-510B-88

Query Match 14.4%; Score 144; DB 1; Length 146;  
Best Local Similarity 33.6%; Pred. No. 2.8e-08;  
Matches 40; Conservative 13; Mismatches 32; Indels 34; Gaps 4;

DB 8 COREKLDMDREMFTEHNGYRAAFARNY-----KTSKMTYVYDC 48  
DB 30 EMKGFDAMRLKFLAHNGYSRLALGHVSITESESDYDLYDSVAPTASKMYRLKYDC 89  
QY 49 TLEKAYSAKCESEPSSE---EENV-----DVSAAITNIPLEAGNSWSEIFEL 97  
DB 90 EAKSAYSAKCKQTTSSTKYDENLVIEDPRDINHAA-----LKAITISMAEARNL 143

RESULT 30  
US-08-458-218-86  
Sequence 86; Application US/08458218  
Patent No. 5789178  
GENERAL INFORMATION:  
APPLICANT: MATTHEW MOYLE ET AL.  
TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS  
NUMBER OF SEQUENCES: 102  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Suite 4700  
STATE: Los Angeles  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
MEDIUM TYPE: storage  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/458,218  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/151,064  
FILING DATE: 10-NOVEMBER-1993  
APPLICATION NUMBER: 08/060,433  
FILING DATE: 11-MAY-1993  
APPLICATION NUMBER: 07/881,721  
FILING DATE: 11-MAY-1992  
APPLICATION NUMBER: 07/996,972  
FILING DATE: 24-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: BIGGS, SUZANNE L.  
REGISTRATION NUMBER: 30,158  
REFERENCE/DOCKET NUMBER: 203/226  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 86:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 146 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
US-08-458-218-86

Query Match 14.4%; Score 144; DB 1; Length 146;  
Best Local Similarity 33.6%; Pred. No. 2.8e-08;  
Matches 40; Conservative 13; Mismatches 32; Indels 34; Gaps 4;

DB 8 COREKLDMDREMFTEHNGYRAAFARNY-----KTSKMTYVYDC 48  
DB 30 EMKGFDAMRLKFLAHNGYSRLALGHVSITESESDYDLYDSVAPTASKMYRLKYDC 89  
QY 49 TLEKAYSAKCESEPSSE---EENV-----DVSAAITNIPLEAGNSWSEIFEL 97  
DB 90 EAKSAYSAKCKQTTSSTKYDENLVIEDPRDINHAA-----LKAITISMAEARNL 143

RESULT 31  
US-08-450-497-88  
Sequence 89; Application US/08450497  
Patent No. 5919800  
GENERAL INFORMATION:  
APPLICANT: MATTHEW MOYLE ET AL.  
TITLE OF INVENTION: NOVEL NEUTROPHIL INHIBITORS  
NUMBER OF SEQUENCES: 104  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Suite 4700  
STATE: Los Angeles  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
MEDIUM TYPE: storage  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,497  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/173,510  
FILING DATE: 23-DEC-1993  
APPLICATION NUMBER: 08/151,064  
FILING DATE: 10-NOV-1993  
APPLICATION NUMBER: 08/060,433





Db 62 WAMCVGFHSPSSSRGICGENYVAWSSGSYRLDKTACT-----DAGRIMNSL-----E 112  
QY 100 KYVN---KNGKTSNTA-----NMWDSHDKLGCAYVDCSGKTH-----VYCO 138  
Db 113 KYISDNSSNMLISEVAMENILHFTOMAMGETYKLG-----SGVDHNIWVARTLVFICH 166  
QY 139 YGPEAKDGKTYIEGAPC-----SRCS 161  
Db 167 YFGGNNYKDLITELGNPKHNKDCRTKRC 197

RESULT 34  
US-08-450-944-2  
Sequence 2, Application US/08450944  
Patent No. 5789194  
GENERAL INFORMATION:  
APPLICANT: TIPP, Cynthia A.  
APPLICANT: Misnewski, Nancy  
TITLE OF INVENTION: PARASTIC HELMINTH VENOM ALLERGEN  
TITLE OF INVENTION: ANTIGEN 5-LIKE GENES AND PROTEINS  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheridan Ross & McIntosh  
STREET: 1700 Lincoln St., Suite 3500  
CITY: Denver  
STATE: Colorado  
COUNTRY: U.S.A.  
ZIP: 80203  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/450,944  
FILING DATE: 23-May-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Vaseer, Carol Talkington  
REGISTRATION NUMBER: 37,459  
REFERENCE/DOCKET NUMBER: 2618-30  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 863-9700  
TELEFAX: (303) 863-0223  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 221 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-450-944-2

Query Match 14.1%; Score 141; DB 1; Length 221;  
Best Local Similarity 27.0%; Pred. No. 1,1e-07;  
Matches 57; Conservative 17; Mismatches 65; Indels 72; Gaps 12;

QY 7 COOREKLDMDREMTFELHNGYRAAFARNY-----KTSKRTVYVDCGLEKAYK 56  
Db 19 CEGGKLTPTERKNIVYQI NKYRSRLRGKLNKDGILMPKGNMLRHRNDCKLEKSAQN 77  
QY 57 SAERC--SEBPSSE-----ENVDF-----SAATLNIPLKAGNSWSEIFELNG 99  
Db 78 WAMCVGFHSPSSSRGICGENYVAWSSGSYRLDKTACT-----DAGRIMNSL-----E 128  
QY 100 KYVN---KNGKTSNTA-----NMWDSHDKLGCAYVDCSGKTH-----VYCO 138  
Db 129 KYISDNSSNMLISEVAMENILHFTOMAMGETYKLG-----SGVDHNIWVARTLVFICH 182  
QY 139 YGPEAKDGKTYIEGAPC-----SRCS 161  
Db 167 YFGGNNYKDLITELGNPKHNKDCRTKRC 213

RESULT 35  
PCT-US96-07709-2  
Sequence 2, Application PC/US9607709  
Patent No. 5958784  
GENERAL INFORMATION:  
APPLICANT: TIPP, Cynthia A.  
APPLICANT: Misnewski, Nancy  
TITLE OF INVENTION: PARASTIC HELMINTH VENOM ALLERGEN  
TITLE OF INVENTION: ANTIGEN 5-LIKE GENES AND PROTEINS  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheridan Ross & McIntosh  
STREET: 1700 Lincoln St., Suite 3500  
CITY: Denver  
STATE: Colorado  
COUNTRY: U.S.A.  
ZIP: 80203  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/07709  
FILING DATE: 23-May-1996  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Connell, Gary J.  
REGISTRATION NUMBER: 32,020  
REFERENCE/DOCKET NUMBER: 2618-30-PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 863-9700  
TELEFAX: (303) 863-0223  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 221 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US96-07709-2

Query Match 14.1%; Score 141; DB 5; Length 221;  
Best Local Similarity 27.0%; Pred. No. 1,1e-07;  
Matches 57; Conservative 17; Mismatches 65; Indels 72; Gaps 12;

QY 7 COOREKLDMDREMTFELHNGYRAAFARNY-----KTSKRTVYVDCGLEKAYK 56  
Db 19 CEGGKLTPTERKNIVYQI NKYRSRLRGKLNKDGILMPKGNMLRHRNDCKLEKSAQN 77  
QY 57 SAERC--SEBPSSE-----ENVDF-----SAATLNIPLKAGNSWSEIFELNG 99  
Db 78 WAMCVGFHSPSSSRGICGENYVAWSSGSYRLDKTACT-----DAGRIMNSL-----E 128  
QY 100 KYVN---KNGKTSNTA-----NMWDSHDKLGCAYVDCSGKTH-----VYCO 138  
Db 129 KYISDNSSNMLISEVAMENILHFTOMAMGETYKLG-----SGVDHNIWVARTLVFICH 182  
QY 139 YGPEAKDGKTYIEGAPC-----SRCS 161  
Db 167 YFGGNNYKDLITELGNPKHNKDCRTKRC 213

RESULT 36  
US-07-857-224B-112  
Sequence 112, Application US/07857224B  
Patent No. 5958784  
GENERAL INFORMATION:  
APPLICANT: Benner, Steven A.  
TITLE OF INVENTION: Predicting Folded Structures of Proteins  
NUMBER OF SEQUENCES: 114  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Steven A. Benner  
STREET: Hadlaubstrasse 151  
CITY: Zurich

STATE: none  
COUNTRY: Switzerland  
ZIP: (note: this is an international post code) CH-8092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 7.0  
SOFTWARE: Microsoft Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/857,224B  
FILING DATE: 03/25/92  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA: none  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (international) 41 1 632 2830  
TELEFAX: (international) 41 1 262 2437  
TELEX: none  
INFORMATION FOR SEQ ID NO: 112:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 138  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
DESCRIPTION: protein  
ORIGINAL SOURCE: human  
ORGANISM: human  
FEATURE: Testis specific protein; Table 17 Row 8  
PUBLICATION INFORMATION:  
AUTHORS:  
AUTHORS: Kaahara, M.  
AUTHORS: Gultnecht, J.  
AUTHORS: Brew, K.  
AUTHORS: Spurr, N.  
AUTHORS: Goodfellow, P. N.  
TITLE: Cloning and mapping of a testis-specific gene with sequence  
TITLE: similarity to a sperm coating glycoprotein gene  
JOURNAL: Genomics  
VOLUME: 5  
PAGES: 527-534  
DATE: 1989  
US-07-857-224B-112

Query Match 12.7%; Score 127; DB 2; Length 138;  
Best Local Similarity 26.9%; Pred. No. 26-06;  
Matches 39; Conservative 23; Mismatches 45; Indels 38; Gaps 8;

QY 38 TSKRTMYVDCITLIE---KAYSAEKSE-----EPSEEVNDVFSATLNIPILEGN 88  
DB 10 TYNAGRWAKCTLOHSDPEDRKSTRGENTYMSDPTS-----MSAI-----Q 54  
QY 89 SWSSEIFELRGKYNNKNGKTSN-----IANWYDSHDKLGCAVYDC---SGKTHVVOY 139  
DB 55 SMTDEILD---YGVGPKSPNAVGHYQLWVSTYVGGLAYCPNGDSLKYVVOY 111  
QY 140 GPEAKGDGK--TIYEGAPCSRCD 162  
DB 112 CPGNNMNRKNTPYQGCTPCAGCPD 136

RESULT 37  
US-08-773-368-4  
Sequence 4, Application US/08773368  
Patent No. 5856130  
GENERAL INFORMATION:  
APPLICANT: Bandman, Olga  
APPLICANT: Goll, Surya K.  
TITLE OF INVENTION: NOVEL HUMAN PATHOGENESIS-RELATED  
TITLE OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto

STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSO for Windows version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/773,368  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy RJ  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0186 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 266 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: Genbank  
CLONE: 1030053  
US-08-773-368-4

Query Match 12.2%; Score 122; DB 2; Length 266;  
Best Local Similarity 24.9%; Pred. No. 1.9e-05;  
Matches 49; Conservative 30; Mismatches 68; Indels 50; Gaps 11;

QY 14 DDDREMFTELHNGRAAFARNYTSKRTMYVDCITLIEKAYSAECS-----EPP- 65  
DB 30 NEDIRKDCVYHNRKRSVRKPT--ASDMLYMTWDPALAQIAWASNCQFSHTRLKPPH 87  
QY 66 -----SSEEN-----VDVFSATLNIPILEGNMSMSEI--FELRGKYNNKNGKTSNIA 112  
DB 88 KLHNFSTLGENIWTGVSPIRSVS-----ATNWYDEIDYDFKTRICK--VCGHYT 139  
QY 113 NMWYDSHDKLGCAVYDC-----SGKTHVVOYGPEAKGDGKT--IYEGAPCSRCD 162  
DB 140 QVWADSVYRGCAQFCPKVSGFDALSNGAHFICNYGP--GNYPTMPYKRGATCSACP 197  
QY 163 YGAGVTCDDDMONILCI 179  
DB 198 -----NDKCLDNLCV 207

RESULT 38  
US-09-199-887-4  
Sequence 4, Application US/09199887  
Patent No. 6071674  
GENERAL INFORMATION:  
APPLICANT: Bandman, Olga  
APPLICANT: Goll, Surya K.  
TITLE OF INVENTION: NOVEL HUMAN PATHOGENESIS-RELATED  
TITLE OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 05/09/199,887  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/773,368  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy R.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0186 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 266 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: Genbank  
CLONE: 1030053  
US-09-199-887-4

Query Match 12.2%; Score 122; DB 3; Length 266;  
Best Local Similarity 24.9%; Pred. No. 1.9e-05;  
Matches 49; Conservative 30; Mismatches 68; Indels 50; Gaps 11;

QY 14 DDDREFFTELHNGYRAAFARANYKTSKRTMYVDCITLEKAYKSAECS-----EEP- 65  
DB 30 NEDIRKCCVIRHNRKFSVKPT--ASDMLYTWDPALQIAKAMASNCQFSHTRLKPPH 87  
QY 66 -----SSEEN-----VDVFSATLNIPILEAGSNWMSI--FELRGKYNNKKGKTSNNA 112  
DB 88 KLHNFSTLGEINMTGSPVIFSVS-----ALTMYDEIDQYKFKRICK--VCGHT 139  
QY 113 NMVDSHDKGCAVYDC-----SGKTHVVCQYGPARGDGT--IYESGAPCSGSD 162  
DB 140 QVWADSYKVGCAVQFCPKVSGFDALNSGAHFICNTP--GNTPTPYRKGATCSACP 197  
QY 163 YGAGVTCDDDMONLCI 179  
DB 198 -----NDKCDNLCV 207

RESULT 39  
US-08-773-368-3  
Sequence 3, Application US/08773368  
Patent No. 5856130  
GENERAL INFORMATION:  
APPLICANT: Bandman, Olga  
APPLICANT: Goll, Surya K.  
TITLE OF INVENTION: NOVEL HUMAN PATHOGENESIS-RELATED  
TIME OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 05/09/199,887  
FILING DATE:  
CLASSIFICATION:

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/773,368  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy R.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0186 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 219 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: Genbank  
CLONE: 847722  
US-08-773-368-3

Query Match 12.1%; Score 121; DB 2; Length 219;  
Best Local Similarity 25.1%; Pred. No. 1.8e-05;  
Matches 49; Conservative 26; Mismatches 74; Indels 46; Gaps 9;

QY 14 DDDREFFTELHNGYRAAFARANYKTSKRTMYVDCITLEKAYKSAECS-----EEP- 65  
DB 20 NEDIRKCCVIRHNRKFSVKPT--ASDMLYTWDPALQIAKAMASNCQFSHTRLKPPH 77  
QY 66 -----SSEEN-----VDVFSATLNIPILEAGSNWMSI--FELRGKYNNKKGKTSNNA 114  
DB 78 KLHNFSTLGEINMTGSPVIFSVS-----ALTMYDEIDQYKFKRICK--VCGHT 131  
QY 115 WVDSDHDKGCAVYDC-----SGKTHVVCQYGPARGDGT--IYESGAPCSGSD 164  
DB 132 QVWADSYKVGCAVQFCPKVSGFDALNSGAHFICNTP--GNTPTPYRKGATCSACP 187  
QY 165 AGVTCDDDMONLCI 179  
DB 188 -----NDKCDNLCV 197

RESULT 40  
US-09-199-887-3  
Sequence 3, Application US/09199887  
Patent No. 6071874  
GENERAL INFORMATION:  
APPLICANT: Bandman, Olga  
APPLICANT: Goll, Surya K.  
TITLE OF INVENTION: NOVEL HUMAN PATHOGENESIS-RELATED  
TIME OF INVENTION: PROTEIN  
NUMBER OF SEQUENCES: 6  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 05/09/199,887  
FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/773,368  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy KJ  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PP-0186 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
TELEX:  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 219 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 847722  
US-09-199-887-3

Query Match 12.1%, Score 121; DB 3; Length 219;  
Best Local Similarity 25.1%, Pred. No. 1.8e-05;  
Matches 49; Conservative 26; Mismatches 74; Indels 9 46; Gaps 9;

QY 14 DDDRMETELHNGRAAFARNTKMTMYDCTLEKAYSAKCS-----EEP- 65  
DB 20 NEDFIDCVRIHNFSEVPT--ASDMLYMTWDPALAQIKAMASNCQFSNTRLKPPH 77  
QY 66 -----SSEEN-----VDVFSATINIPLEAGNSWSEIFELRGVYRNKNGKTSINAM 114  
DB 78 KLHPNTSGENIMTVGSVPIFSVS-----ATNMYDEIQDNFTYRICKVYCGHYOV 131  
QY 115 VMDSHKLCAVAVDC-----SGKTHVCOYGPFAKGGGT--TYEGACSCSCSYG 164  
DB 132 VMADSKYCAVQPCPKVSGFDALSNAGHFIQNGP--GNYPTWPKKAGATCSAPN-- 187  
QY 165 AGVTCDDDMQNLICI 179  
DB 188 ----NDKCLDNLICV 197

RESULT 41  
US-07-857-224B-111  
Sequence 111, Application US/07857224B  
Patent No. 5958784  
GENERAL INFORMATION:  
APPLICANT: Bennett, Steven A.  
TITLE OF INVENTION: Predicting Folded Structures of Proteins  
NUMBER OF SEQUENCES: 114  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Steven A. Bennett  
STREET: Hadlaubstrasse 151  
CITY: Zurich  
STATE: none  
COUNTRY: Switzerland  
ZIP: (note: this is an international post code) CH-8092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette, 1.4 Mb storage  
OPERATING SYSTEM: Macintosh 7.0  
SOFTWARE: Microsoft Word  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/857,224B  
FILING DATE: 03/25/92  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (international) 41 1 632 2830  
TELEFAX: (international) 41 1 262 2437  
TELEX: none  
INFORMATION FOR SEQ ID NO: 111:

SEQUENCE CHARACTERISTICS:  
LENGTH: 137  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
DESCRIPTION: protein  
ORIGINAL SOURCE:  
ORGANISM: human  
FEATURE: testis specific protein; Table 17 Row 7  
PUBLICATION INFORMATION:  
AUTHORS:  
AUTHORS: Kasahara, M.  
AUTHORS: Gutknecht, J.  
AUTHORS: Brew, K.  
AUTHORS: Spurr, N.  
AUTHORS: Goodfellow, P. N.  
TITLE: Cloning and mapping of a testis-specific gene with sequence  
TITLE: similarity to a sperm coating glycoprotein gene  
JOURNAL: Genomics  
VOLUME: 5  
PAGES: 527-534  
DATE: 1989  
US-07-857-224B-111

Query Match 11.5%, Score 115; DB 2; Length 137;  
Best Local Similarity 28.0%, Pred. No. 4.2e-05;  
Matches 35; Conservative 19; Mismatches 49; Indels 22; Gaps 6;

QY 54 AYKAERKSEPSSEENVDFSAATINIPLEAGNSWSEIFELRGVYRNK-----G 106  
DB 13 AQKANKCLIEHSSDDR-KINIRGENTLWSTPTLWSTYIQ---SWYNEDDFYVVG 68  
QY 107 KTSIA-----NMVDSHDKLCAVDCSGKTHV---VCOYGEAGGDK--TYEBSA 155  
DB 69 AKPSAVGHYQVWYSSFKIGCIACVCPQDRLKYFYVCHYCPWGNVVKKSTPYQGT 128  
QY 156 PCSRC 160  
DB 129 PCASC 133

RESULT 42  
US-08-614-935-5  
Sequence 5, Application US/08614935  
Patent No. 5804201  
GENERAL INFORMATION:  
APPLICANT: King, Te P.  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES OF VESPID  
NUMBER OF SEQUENCES: 81  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: David A. Jackson, Esq.  
STREET: 411 Hackensack Ave, Continental Plaza, 4th  
STREET: Floor  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/614,935  
FILING DATE: 11-MAR-1996  
CLASSIFICATION: 436  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-156  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-487-5800

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? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? HYPOTHEITICAL: NO
? ANTI-SENSE: NO
? FRAGMENT TYPE:
? ORIGINAL SOURCE:
? ORGANISM: Dolichovespula maculata
? US-09-130-287-5

Query Match      11 %; Score 112.5; DB 3; Length 204;
Best Local Similarity 23.4%; Pseq. No. 0.00014;
Matches 33; Conservative 27; Mismatches 74; Indels 27; Gaps 6

OY      13 LDDDKREFETLHNGRPAFANKT-----SKRTMYDCTLEKAYSAKC- 61
DB      36 LTDEKNELTLKRHDNRQVNAGLETKGCGQPAPKKNNVLWNDELKLNQWACD 95
OY      62 -----SEEPSSEENVDS--AATNLPIBAGNSMSEIFELGKYKNG--KTS 109
DB      96 FHHDCORTARYQYGGINAISSTATQFDPSRLKLKQWEDVEEFYFKGLQNSFRKG 155
OY      110 NIANVMYSDHDLCA--VVDCSGKTH-VQCYSPKASGDGTIVE 152
DB      156 HTOMWGMKTKEIGCSIXIYIEDNWMYHYLVANCYGGNDPNPDIYE 202

RESULT 44
US-08-614-935-4
Sequence 4, Application US/08614935
Patent No. 5804201
GENERAL INFORMATION:..
APPLICANT: KING, Te P.
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES OF VESPID
TITLE OF INVENTION: ANTIGEN 5
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
FLOOR
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/614.935
FILING DATE: 11-MAR-1996
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1156
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 205 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEITICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: Dolichovespula maculata
? US-08-614-935-4
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Query Match	11.0%;	Score 110;	DB 1;	Length 205;
Best Local Similarity	23.4%;	Pred. No. 0.00027;		
Matches 40;	Conservative 30;	Mismatches 67;	Indels 34;	Gaps 8;

QY 13 LDDDMKEMTLEHNGYGAFAARYYKT-----SKRTVYDCLELKAFAKSEKCS 62  
 Db 36 VSDMEKNEIYVNHQOPROKVAKLETRBNPPOPAPKANNVYVWMDLAKIAOTANQCS 95  
 QY 63 -----EPESEBENVDFESA-----ATNLEPLEAGSNMSEITFEL---RRTKYNN- 109  
 Db 96 FGDHOCRNTEKQYGVQVVALASTNSVATMSKILE---MMEENKOPNPKKOTIGDNF 123  
 QY 106 GKTSNLIANNWDSBDKGA---VYDCSGRTH--VNGQVPEPAKDGKTYIE 152  
 Db 153 SKRGHTTQVMMOKTKREIGCSVATYENNMHHITLCVTCISPAQNTADDPILIE 203

RESULT 45  
PS-09-130

US-09-130-287-4  
; Sequence 4, Application US/09130287  
; Patent No. 510694

GENERAL INFORMATION:

APPLICANT: King, Te P.  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES OF VESPID  
CLASS OF INVENTION: IMMUNOMODULATORY PEPTIDES

CORRESPONDENCE ADDRESS:

ADDRESS: David A. Jackson, Esq.  
STREET: 411 Hackensack Ave, Continental Plaza, 4th  
CITY: New York

COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: DOS 3.3

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SOFTWARE: PatentIn Release #1.0, Version #1.30
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APPLICATION NUMBER: US/09/130,287

CLASSIFICATION: 424

APPLICATION NUMBER:

CLASSIFICATION: 424

NAME: Jackson Esq., David A.

REFERENCE/DOCKET NUMBER: 600-1-15

TELEPHONE: 201-487-5800

; INFORMATION FOR SEQ ID NO

LENGTH: 205 amino acids

STRANDEDNESS: single

MOLECULE TYPE: protein

ANTI-SENSE: NO

ORIGINAL SOURCE:

US-09-130-287-4

Query Match	11.08; Score 1
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Matches 40; Conservative 30; Mismatches 20; Conservative 10; Mismatches 10

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0Y      13 LDDMMEMFTELHNGYVPAAFARNYK-----SKMTWYCYCTLEAKVSAEKXS   62
           :|::||::||::||::||::||::||::||::||::||::||::||::||::||
Db     36 VSNDEKNELVNNHHNOFORKAKCLETRGCPQPPARKNNVNVLMNDELAKIAOTMANOCS   95
           :|::||::||::||::||::||::||::||::||::||::||::||::||
0Y      63 -----EPESEEEENVADFEA-----ATNTIDLEAGNSMWSSEIFEL---RGCVYNNK-   10
           :|::||::||::||::||::||::||::||::||::||::||::||::||
Db     96 FGHDOCRNFKEVOYGQVVVAIASTTGSVSATMSKLIE---KMEENPKVDNPBKGTGDONNE   15
           :|::||::||::||::||::||::||::||::||::||::||::||::||
0Y      106 GKHSNIANNVWMDSHDKTGCA---VYDSCGRTH-VYCOCYPEAKSGKGITYE   152
           :|::||::||::||::||::||::||::||::||::||::||::||::||
Db     153 SKYGHYTKVMWKETKEIGCGSVKYLIENNHHHYLCYCNPSAGBYWDQDYITE   203
           :|::||::||::||::||::||::||::||::||::||::||::||::||

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Search completed: July 15, 2003, 08:36:45  
Job time : 28 secs

Tue Jul 15 09:48:47 2003

us-09-937-555a-2.rapb

Page 1

GenCore version 5.1.6  
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OW protein - protein search, using sw model

Run on: July 15, 2003, 08:32:48 ; Search time 23 Seconds  
(without alignments)  
916.173 Million cell updates/sec

Title: US-09-937-555a-2  
Perfect score: 997  
Sequence: 1 BGDYSLCQREKLDMDRMK.....DYAGVTCDDDMQNLICGH 181

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 445758 seqs, 116419773 residues

Total number of hits satisfying chosen parameters: 445758

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:  
1: /cgn2\_6/p/cdata/1/pubpa/US07\_NEW\_PUB.pep.\*  
2: /cgn2\_6/p/cdata/1/pubpa/PC1\_NEW\_PUB.pep.\*  
3: /cgn2\_6/p/cdata/1/pubpa/US06\_PUBCOMB.pep.\*  
4: /cgn2\_6/p/cdata/1/pubpa/PC0US\_PUBCOMB.pep.\*  
5: /cgn2\_6/p/cdata/1/pubpa/US07\_PUBCOMB.pep.\*  
6: /cgn2\_6/p/cdata/1/pubpa/US08\_PUBCOMB.pep.\*  
7: /cgn2\_6/p/cdata/1/pubpa/US09\_PUBCOMB.pep.\*  
8: /cgn2\_6/p/cdata/1/pubpa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/p/cdata/1/pubpa/US09\_PUBCOMB.pep.\*  
10: /cgn2\_6/p/cdata/1/pubpa/US10\_NEW\_PUB.pep.\*  
11: /cgn2\_6/p/cdata/1/pubpa/US10\_PUBCOMB.pep.\*  
12: /cgn2\_6/p/cdata/1/pubpa/US60\_PUBCOMB.pep.\*  
13: /cgn2\_6/p/cdata/1/pubpa/US60\_PUBCOMB.pep.\*  
14: /cgn2\_6/p/cdata/1/pubpa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	290	29.1	257	10	US-09-969-271-4
2	290	29.1	257	10	US-09-969-271-3
3	290	29.1	274	10	US-09-969-271-3
4	290	29.1	274	10	US-09-969-271-3
5	290	29.1	274	10	US-09-969-271-3
6	290	29.1	274	10	US-09-969-271-3
7	290	29.1	274	10	US-09-969-271-3
8	290	29.1	274	10	US-09-969-271-3
9	290	29.1	274	10	US-09-969-271-3
10	290	29.1	274	10	US-09-969-271-3
11	290	29.1	274	10	US-09-969-271-3
12	290	29.1	274	10	US-09-969-271-3
13	290	29.1	274	10	US-09-969-271-3
14	290	29.1	274	10	US-09-969-271-3
15	290	29.1	274	10	US-09-969-271-3
16	290	29.1	274	10	US-09-969-271-3
17	290	29.1	274	10	US-09-969-271-3
18	290	29.1	274	10	US-09-969-271-3
19	290	29.1	274	10	US-09-969-271-3

20	159	15.9	463	9	US-09-906-838-285	Sequence 285, App
21	159	15.9	463	9	US-09-907-613-285	Sequence 285, App
22	159	15.9	463	9	US-09-907-942-285	Sequence 285, App
23	159	15.9	463	9	US-10-175-746-360	Sequence 360, App
24	159	15.9	463	9	US-10-176-918-360	Sequence 360, App
25	159	15.9	463	9	US-10-176-921-360	Sequence 360, App
26	159	15.9	463	9	US-10-137-865-360	Sequence 360, App
27	159	15.9	463	9	US-10-140-474-360	Sequence 360, App
28	159	15.9	463	9	US-09-904-859-285	Sequence 285, App
29	159	15.9	463	9	US-09-904-859-285	Sequence 285, App
30	159	15.9	463	9	US-09-909-204-285	Sequence 285, App
31	159	15.9	463	9	US-10-142-431-360	Sequence 360, App
32	159	15.9	463	9	US-10-143-114-360	Sequence 360, App
33	159	15.9	463	9	US-09-904-786-285	Sequence 285, App
34	159	15.9	463	9	US-09-906-646-285	Sequence 285, App
35	159	15.9	463	9	US-09-906-700-285	Sequence 285, App
36	159	15.9	463	9	US-09-902-903-285	Sequence 285, App
37	159	15.9	463	9	US-09-903-749-285	Sequence 285, App
38	159	15.9	463	9	US-09-903-749-285	Sequence 285, App
39	159	15.9	463	9	US-09-902-903-285	Sequence 285, App
40	159	15.9	463	9	US-10-142-419-360	Sequence 360, App
41	159	15.9	463	9	US-09-902-903-285	Sequence 285, App
42	159	15.9	463	9	US-09-902-903-285	Sequence 285, App
43	159	15.9	463	9	US-09-904-786-285	Sequence 285, App
44	159	15.9	463	9	US-09-904-786-285	Sequence 285, App
45	159	15.9	463	9	US-10-123-262-360	Sequence 360, App

ALIGNMENTS

RESULT 1  
US-09-969-271-4  
Sequence 4, Application US/09969271  
Patent No. US20020098179A1  
GENERAL INFORMATION:  
APPLICANT: Pfizer, Inc. (All designated States except GB and EP (GB) only)  
INVENTOR: Pfizer, Inc. (All designated States except GB and EP (GB) only)  
TITLE OF INVENTION: PCS1091APME  
FILE REFERENCE: PCS1091APME  
CURRENT FILING DATE: 2001-10-01  
PRIORITY FILING DATE: 2000-10-17  
PRIORITY FILING DATE: 2000-10-17  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: PASTSEQ for Windows Version 4.0  
SEQ ID NO: 4  
LENGTH: 257  
ORIGIN: Ancylostoma caninum (canine hookworm)  
ORIGIN: Ancylostoma caninum (canine hookworm)  
US-09-969-271-4

Query Match 29.1%; Score 290; DB 10; Length 257;  
Best Local Similarity 34.3%; Pred. No. 4.3e-21;  
Matches 69; Conservative 23; Mismatches 57; Indels 52; Gaps 7;

QY	14	DDDKREKTEHNGYRAAFVARNY	-----KTSKRMVYDCL 50
DB	18	NDSTRLQPLAHNGYRSKLAALHSITESESDDDDFGLPDPAPRSKRLIEDCA 77	
QY	51	EKKAVKSKKCSDE--PSSEENVDFSAFLNT---PLENGSWSEIFEL-----R 98	
DB	78	EKSAYNSARNCSDESSPPGKYDENTYFENSN-NISBAALAKMISMAKFAFNKTKKEE 136	
QY	99	GAYTKKRNKTSNLANVWDSHDKLCAVADC-----SCT-----HYVCOGPE 142	
DB	137	GVLYSNNDINFNANLAWDAKRFCAVAVNCPLOEIDETNHDGELVITTHVCHPRT 196	
QY	143	AKGDGKTYEDGAPCSRSDY 163	
DB	197	NKTEGQPIYKVTGTCDDCSEY 217	

RESULT 2  
US-09-797-410-3  
Sequence 3, Application US/09797410  
Patent No. US20020099183A1  
GENERAL INFORMATION:  
APPLICANT: Pluschell, Stefanie B.  
APPLICANT: Geldart, Roderick W.  
APPLICANT: Ho, Lewis  
APPLICANT: Koehler, Mark A.  
APPLICANT: Okedadi, Centry A.  
APPLICANT: Plas, Steven J.  
APPLICANT: Zhu, Marie M.  
TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF NEUTROPHIL INHIBITORY  
FILE REFERENCE: SUZANNE L. BIGGS: Corvas 259/001  
CURRENT APPLICATION NUMBER: US/09/797,410  
CURRENT FILING DATE: 2001-02-28  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 3  
LENGTH: 257  
TYPE: PRT  
ORGANISM: Ancylostoma caninum  
FEATURE:  
NAME/KEY: PEPTIDE  
LOCATION: (1)..(257)  
US-09-797-410-3  
Query Match 29.1%; Score 290; DB 10; Length 257;  
Best Local Similarity 34.3%; Pred. No. 4.3e-21;  
Matches 69; Conservative 23; Mismatches 57; Indels 52; Gaps 7;  
DB 14 DDREKFEFLHNGYRAAFARNY-----KTSKRMVYDCTL 50  
18 NDSIRLOFLAHNGYRSKLAIGHISTEESDDDDDFGLPDPAPRASKRMYLEDCBA 77  
51 EKAYKSAKSCSE---PSSEENVDFSAATLNT---PLEAGNSMSEIFEL-----R 98  
78 EKAYNSARNCSDSSSPPEGDYENKTYIFENS-NISEALKAMISMAREAFNLNKTKEGE 136  
99 GKYVNRKNGKTSNINAMVWDSDHDKLCAYVDC-----SGKT-----HYVCOYGE 142  
137 GYLRSNHDISNFAANLAMDAREKFCGAVVNCPLGEIDETNHDGETATYTIHVCHYPR 196  
QY 143 AKGDKITYEKGAPCSRCSY 163  
DB 197 NTEGQPIYKVGTPCDDCSEY 217  
RESULT 3  
US-09-969-271-3  
Sequence 3, Application US/09969271  
Patent No. US20020098179A1  
GENERAL INFORMATION:  
APPLICANT: Pfizer Inc. (All designated States except GB and EP (GB));  
APPLICANT: Pfizer Limited (GB and EP (GB) only)  
TITLE OF INVENTION: Pharmaceutical Combinations  
FILE REFERENCE: PCS10951APPE  
CURRENT APPLICATION NUMBER: US/09/969,271  
CURRENT FILING DATE: 2001-10-01  
PRIOR APPLICATION NUMBER: GB 005473.0  
PRIOR FILING DATE: 2000-10-17  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 274  
TYPE: PRT  
ORGANISM: Ancylostoma caninum (canine hookworm)  
US-09-969-271-3  
Query Match 29.1%; Score 290; DB 10; Length 274;  
Best Local Similarity 34.3%; Pred. No. 4.7e-21;  
Matches 69; Conservative 23; Mismatches 57; Indels 52; Gaps 7;

QY 14 DDREKFEFLHNGYRAAFARNY-----KTSKRMVYDCTL 50  
DB 35 NDSIRLOFLAHNGYRSKLAIGHISTEESDDDDDFGLPDPAPRASKRMYLEDCBA 94  
QY 51 EKAYKSAKSCSE---PSSEENVDFSAATLNT---PLEAGNSMSEIFEL-----R 98  
DB 95 EKAYNSARNCSDSSSPPEGDYENKTYIFENS-NISEALKAMISMAREAFNLNKTKEGE 153  
QY 99 GKYVNRKNGKTSNINAMVWDSDHDKLCAYVDC-----SGKT-----HYVCOYGE 142  
DB 154 GYLRSNHDISNFAANLAMDAREKFCGAVVNCPLGEIDETNHDGETATYTIHVCHYPR 213  
QY 143 AKGDKITYEKGAPCSRCSY 163  
DB 214 NTEGQPIYKVGTPCDDCSEY 234  
RESULT 4  
US-09-797-410-2  
Sequence 2, Application US/09797410  
Patent No. US20020099183A1  
GENERAL INFORMATION:  
APPLICANT: Pluschell, Stefanie B.  
APPLICANT: Geldart, Roderick W.  
APPLICANT: Ho, Lewis  
APPLICANT: Koehler, Mark A.  
APPLICANT: Okedadi, Centry A.  
APPLICANT: Plas, Steven J.  
APPLICANT: Zhu, Marie M.  
TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF NEUTROPHIL INHIBITORY  
FILE REFERENCE: SUZANNE L. BIGGS: Corvas 259/001  
CURRENT APPLICATION NUMBER: US/09/797,410  
CURRENT FILING DATE: 2001-02-28  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 2  
LENGTH: 274  
TYPE: PRT  
ORGANISM: Ancylostoma caninum  
US-09-797-410-2  
Query Match 29.1%; Score 290; DB 10; Length 274;  
Best Local Similarity 34.3%; Pred. No. 4.7e-21;  
Matches 69; Conservative 23; Mismatches 57; Indels 52; Gaps 7;  
DB 14 DDREKFEFLHNGYRAAFARNY-----KTSKRMVYDCTL 50  
35 NDSIRLOFLAHNGYRSKLAIGHISTEESDDDDDFGLPDPAPRASKRMYLEDCBA 94  
QY 51 EKAYKSAKSCSE---PSSEENVDFSAATLNT---PLEAGNSMSEIFEL-----R 98  
DB 95 EKAYNSARNCSDSSSPPEGDYENKTYIFENS-NISEALKAMISMAREAFNLNKTKEGE 153  
QY 99 GKYVNRKNGKTSNINAMVWDSDHDKLCAYVDC-----SGKT-----HYVCOYGE 142  
DB 154 GYLRSNHDISNFAANLAMDAREKFCGAVVNCPLGEIDETNHDGETATYTIHVCHYPR 213  
QY 143 AKGDKITYEKGAPCSRCSY 163  
DB 214 NTEGQPIYKVGTPCDDCSEY 234  
RESULT 5  
US-10-051-644B-6  
Sequence 6, Application US/10051644B  
Publication No. US20030126625A1  
GENERAL INFORMATION:  
APPLICANT: Liu, et al.  
TITLE OF INVENTION: Screens and Assays for Agents Useful in Controlling  
FILE REFERENCE: 2002630-0012



```

; CURRENT APPLICATION NUMBER: US/10/051,644B
; CURRENT FILING DATE: 2003-03-04
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Clustal W
; OTHER INFORMATION: Alignment of VAP-1, VAP-2, and selected other
; OTHER INFORMATION: nematode VA Proteins.
US-10-051-644B-6

Query Match
Best Local Similarity 25.68; Score 255; DB 9; Length 205;
Matches 62; Conservative 27; Mismatches 70; Indels 32; Gaps 7;

QY 7 CQOREKIDDDREMTFELANGYRAAFARNY-----KTSKRTVYDCTLEEKAYK 56
DB 9 CPSNTGMTDSVDTFL-VHNEFRSSVANGLEPPDLAGSNAPKAKMLKKVYDCEVSAIR 67
QY 57 SAERCSSEPSSEEE---NVDFSAATLNI-----PLEAGNSMSEIFE-----LKG 99
DB 66 HONKCVYOHSHGEDRGLENTYKTSYKFDKXNAKQAQSLMWNLEKEFGVPSNLT 127
QY 100 KYTNKNG-KTSNIANNVMDSHDKGCAVYDSCGKTHVYCGYGPPEAGDKTYEEGAPCS 158
DB 128 ALMNPQMGIQHYTOMAMDTYKLGCAVYGCNPFTEGVCQYGPAGNYMGHYITMGOPCS 187
QY 159 RCDSDYGAGVTC 169
DB 188 QCS---PGATC 195

RESULT 6
US-10-051-644B-3
; Sequence 3, Application US/10051644B
; Publication No. US20030126625A1
; GENERAL INFORMATION:
; APPLICANT: Liu, et al.
; TITLE OF INVENTION: Screens and Assays for Agents Useful in Controlling
; FILE REFERENCE: 2002630-0012
; CURRENT APPLICATION NUMBER: US/10/051,644B
; CURRENT FILING DATE: 2003-03-04
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VAP-2 Amino
; OTHER INFORMATION: Acid Sequence
US-10-051-644B-3

Query Match
Best Local Similarity 21.08; Score 209.5; DB 9; Length 473;
Matches 59; Conservative 26; Mismatches 87; Indels 45; Gaps 7;

QY 6 LCOOREKIDDD-----KREMTFELANGYRAAFARNY-----KTSK 40
DB 256 LCAQPSWYVDDGSGCQNSLYSVTINFTLEQHNFTSLKAGFEWNGETNTSOPKASQ 315
QY 41 MRYVYDCTLEEKAYKSEK-----SEPSSEENVDFSAAT--LNIPLAGNSMW 91
DB 316 MKEKIDCTLEKRNPNANNCVFNHSAHYERPNQONLYMSFSNPPRSLHTHTAVEKMW 375
QY 92 SEIFE-----LNGKYTNKNGKT-SNIANNVMDSHDKGCAVYDSCGKTHVYCGYGP 142
DB 376 QELEREGTIDVNLTPLELMDLKGAKAGHYTOMAMDTYKLGCIANGCPKMSYVCHYGP 435
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QY 143 AKGDGKTYEEGAPCSRCSRDYAGVTCDDDMQNLICI 179
DB 436 GNRRNKKIYEIGDDPCENVDDCPIDGDCER--TTSICV 470

RESULT 7
US-10-051-644B-1
; Sequence 1, Application US/10051644B
; Publication No. US20030126625A1
; GENERAL INFORMATION:
; APPLICANT: Liu, et al.
; TITLE OF INVENTION: Screens and Assays for Agents Useful in Controlling
; FILE REFERENCE: 2002630-0012
; CURRENT APPLICATION NUMBER: US/10/051,644B
; CURRENT FILING DATE: 2003-03-04
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VAP-1 Amino
; OTHER INFORMATION: Acid Sequence
US-10-051-644B-1

Query Match
Best Local Similarity 19.18; Score 190; DB 9; Length 425;
Matches 45; Conservative 40; Mismatches 79; Indels 32; Gaps 5;

QY 4 YSLCQOREKIDDDREMTFELANGYRAAFARNYKTSK-----RTMYDCTL 50
DB 222 FVWCPSVYDQSDQARQNFLDTHNKLKTSILAKLEADGAIAGAPAPAKOMPLRYKISCTV 281
QY 51 EEKAYKSAERCSSEPSSEEE---NVDFSAATLNIPL-----EAGNSMSEIFE----- 96
DB 282 ENAKRTAKKGLYHSTSAQRPELGENTLWISINNMFKIOTARDSSKAWMSLKDPEVGS 341
QY 97 ---LNGKYTNKNGKTSNIANNVMDSHDKGCAVYDSCGKTHVYCGYGPANQDKTYEE 153
DB 342 DNLITQAVFDG--VGHYTOMAMEGTTEIGCEVENCPTFTYSVCQYGPAGNYMQLIYTK 399
QY 154 GAPCSRCSRDYAGVTC 169
DB 400 GSECTRADDCPGTQTC 415

RESULT 8
US-09-808-602-27
; Sequence 27, Application US/09808602
; Patent No. US2002015115A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A
; APPLICANT: Fernandes, Elma
; APPLICANT: Shinkels, Richard A
; APPLICANT: Herrman, John L
; APPLICANT: Majumder, Kumud
; APPLICANT: Mishra, Yashu
; APPLICANT: Mezes, Peter S
; APPLICANT: MacDougall, John
; TITLE OF INVENTION: No. US2002015115A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-697 CIP
; CURRENT APPLICATION NUMBER: US/09/808,602
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 09/800,198
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/186,596
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 300
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TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-808-602-27

Query Match 15.0%: Score 160; DB 9; Length 300;  
Best Local Similarity 25.5%: Pred. No. 5.3e-08;  
Matches 53; Conservative 31; Mismatches 66; Indels 58; Gaps 11;

QY 1 EGDYSLCOOREK---LDDMEKMETELANGYRAAFANRKT-SKARTMYDCTLEKAYK 56  
DB 43 DGEWMIMKOKRKRAITDNDQSI-L-DHANKLR---SQYTPASNNEYTWVDLEERSAS 98  
QY 57 SAERKCEEE-PSSEENVDVSAATLNIPLEAG-----NSWSEI----- 94  
DB 99 RAESCMEHGPAS-----LPSIGQNLGAHMGRTPRPEHVQSWYDEVDSFYREHC 152  
QY 95 -----FELRGKYNNKGTSTNIAMVDSHDKLGCAVYDCSG-----KTHVVCQY 139  
DB 153 NPYCFPCSGPV-----CTHYTVVATSNRIGCAINLCHNNIMWQIWPRAVYLVCNY 206  
QY 140 GPEAKGDGKTYEEGAPCSR-SDYGAG 166  
DB 207 SPKGNMNGHAPYKHGRPCSPSPSGCG 234

## RESULT 9

US-09-800-198-25  
Sequence 25, Application US/09800198  
Publication No. US20030087816A1  
GENERAL INFORMATION:  
APPLICANT: Vernet, Corlie AM  
APPLICANT: Fernandes, Elma  
APPLICANT: Shinkels, Richard A  
APPLICANT: Hermann, John L  
APPLICANT: Majumder, Kumud  
APPLICANT: Mishra, Vishna  
APPLICANT: Mezes, Peter S  
APPLICANT: Raetelli, Luca  
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
FILE REFERENCE: 15966-697  
CURRENT FILING DATE: 2001-07-12  
CURRENT APPLICATION NUMBER: US/09/800,198  
PRIOR FILING DATE: 2001-03-05  
PRIOR APPLICATION NUMBER: 60/146,596  
NUMBER OF SEQ ID NOS: 98  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 25  
LENGTH: 300  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-800-198-25

Query Match 16.0%: Score 160; DB 9; Length 300;  
Best Local Similarity 25.5%: Pred. No. 5.3e-08;

Matches 53; Conservative 31; Mismatches 66; Indels 58; Gaps 11;

QY 1 EGDYSLCOOREK---LDDMEKMETELANGYRAAFANRKT-SKARTMYDCTLEKAYK 56  
DB 43 DGEWMIMKOKRKRAITDNDQSI-L-DHANKLR---SQYTPASNNEYTWVDLEERSAS 98  
QY 57 SAERKCEEE-PSSEENVDVSAATLNIPLEAG-----NSWSEI----- 94  
DB 99 RAESCMEHGPAS-----LPSIGQNLGAHMGRTPRPEHVQSWYDEVDSFYREHC 152  
QY 95 -----FELRGKYNNKGTSTNIAMVDSHDKLGCAVYDCSG-----KTHVVCQY 139  
DB 153 NPYCFPCSGPV-----CTHYTVVATSNRIGCAINLCHNNIMWQIWPRAVYLVCNY 206  
QY 140 GPEAKGDGKTYEEGAPCSR-SDYGAG 166  
DB 207 SPKGNMNGHAPYKHGRPCSPSPSGCG 234

## RESULT 10

US-09-905-291A-285  
Sequence 285, Application US/09905291A  
Patent No US20020160374A1

GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Dotschtein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kjaevn, Ivar J.  
APPLICANT: Kjaevn, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: 10466-14  
CURRENT FILING DATE: 2001-07-12  
CURRENT APPLICATION NUMBER: US/09/905,291A  
PRIOR FILING DATE: 2001-07-12  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 285  
LENGTH: 463  
TYPE: PRT

ORGANISM: Homo Sapien  
US-09-905-291A-285

Query Match 15 98; Score 159; DB 9; Length 463;  
Best Local Similarity 28.68; Pred. No. 1.2e-07;  
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;

OY 13 LDDDKREFTLHNGYAAAFARNTKSKRTVYDCTLEKAYKSAKC---SEPSSE 68  
DB 28 LIDDKRLMVELHNLVLAQVSP--ASDLHMRDEELAAFAKAYAROCVMGHNKERGR 85  
OY 69 EENVDFSAATLNTLEAGNSWSEIFELRGKRYNKNKTSNTANM-----VWDSHK 121  
DB 86 GENLPAITDEGMDVPL-AMEEMHE-----REHNLSAATCSFGQMGCHYTQVWAKTER 139  
OY 122 LGCAYVDCS-----GKTHV---VCQYGPBAGDKGTIYEGAPCSRCSDYAGVTCDDW 173  
DB 140 ICGSGHFEEKLOGVEETINIELVNCNEPPGVNKGKRPYQBSTPCSCP---SGYHC--- 192  
OY 174 QNLIC 178  
DB 193 KNSLC 197

RESULT 11  
US-09-902-853-285  
Sequence 285, Application US/09902853  
Publication No. US20020192659A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Grimaldi, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavita, Ivar J.  
APPLICANT: Mathew, Jennie P.  
APPLICANT: Pao, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumes, Daniel  
APPLICANT: Williams, P.  
APPLICANT: Wood, William, I.  
TIME OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TIME OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: 1066-14  
CURRENT APPLICATION NUMBER: US/09/902, 853  
PRIOR APPLICATION NUMBER: US/00-07-10  
PRIOR FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: US 60/143, 350  
PRIOR FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: US 60/143, 048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145, 698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146, 222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 285  
LENGTH: 463  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-09-902-853-285

Query Match 15 98; Score 159; DB 9; Length 463;  
Best Local Similarity 28.68; Pred. No. 1.2e-07;  
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;

OY 13 LDDDKREFTLHNGYAAAFARNTKSKRTVYDCTLEKAYKSAKC---SEPSSE 68  
DB 28 LIDDKRLMVELHNLVLAQVSP--ASDLHMRDEELAAFAKAYAROCVMGHNKERGR 85  
OY 69 EENVDFSAATLNTLEAGNSWSEIFELRGKRYNKNKTSNTANM-----VWDSHK 121  
DB 86 GENLPAITDEGMDVPL-AMEEMHE-----REHNLSAATCSFGQMGCHYTQVWAKTER 139  
OY 122 LGCAYVDCS-----GKTHV---VCQYGPBAGDKGTIYEGAPCSRCSDYAGVTCDDW 173  
DB 140 ICGSGHFEEKLOGVEETINIELVNCNEPPGVNKGKRPYQBSTPCSCP---SGYHC--- 192  
OY 174 QNLIC 178  
DB 193 KNSLC 197

RESULT 12  
US-09-907-824-285  
Sequence 285, Application US/09907824  
Publication No. US20020197671A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerltsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavita, Ivar J.  
APPLICANT: Mathew, Jennie P.  
APPLICANT: Pao, James  
APPLICANT: Paoni, Nicholas F.

```

/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tunes, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William, I.
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE REFERENCE: 10466-14
/ CURRENT APPLICATION NUMBER: US/09/907,824
/ PRIOR APPLICATION NUMBER: 2001-07-17
/ PRIOR APPLICATION NUMBER: 2000-09-18
/ PRIOR APPLICATION NUMBER: PCT/US00/04414
/ PRIOR FILING DATE: 2000-02-22
/ PRIOR APPLICATION NUMBER: US 60/143,048
/ PRIOR FILING DATE: 1999-07-07
/ PRIOR APPLICATION NUMBER: US 60/145,698
/ PRIOR FILING DATE: 1999-07-26
/ PRIOR APPLICATION NUMBER: US 60/146,222
/ PRIOR FILING DATE: 1999-07-28
/ PRIOR APPLICATION NUMBER: PCT/US99/20594
/ PRIOR FILING DATE: 1999-09-08
/ PRIOR APPLICATION NUMBER: PCT/US99/20944
/ PRIOR FILING DATE: 1999-09-13
/ PRIOR APPLICATION NUMBER: PCT/US99/21090
/ PRIOR FILING DATE: 1999-09-15
/ PRIOR APPLICATION NUMBER: PCT/US99/21547
/ PRIOR FILING DATE: 1999-09-15
/ PRIOR APPLICATION NUMBER: PCT/US99/23089
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: PCT/US99/28214
/ PRIOR FILING DATE: 1999-11-29
/ PRIOR APPLICATION NUMBER: PCT/US99/28313
/ PRIOR FILING DATE: 1999-11-30
/ PRIOR APPLICATION NUMBER: PCT/US99/28564
/ PRIOR FILING DATE: 1999-12-02
/ PRIOR APPLICATION NUMBER: PCT/US99/28565
/ PRIOR FILING DATE: 1999-12-02
/ PRIOR APPLICATION NUMBER: PCT/US99/30095
/ PRIOR FILING DATE: 1999-12-16
/ PRIOR APPLICATION NUMBER: PCT/US99/30911
/ PRIOR FILING DATE: 1999-12-20
/ PRIOR APPLICATION NUMBER: PCT/US99/30999
/ PRIOR FILING DATE: 1999-12-20
/ PRIOR APPLICATION NUMBER: PCT/US00/00219
/ PRIOR FILING DATE: 2000-01-05
/ NUMBER OF SEQ ID NOS: 423
/ SEQ ID NO 285
/ LENGTH: 463
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-09-907-824-285

Query Match      15.9%; Score 159; DB 9; Length 463;
Best Local Similarity 28.6%; Pred. No. 1.2e-07;
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;

QY 13 LDDDMREMFELHNGRAAFARNTKTSKMTVYDCTLEKAYKSAKRC-----SEPPSSE 68
DB 28 LTDEKRLAYELHNLRYAQSPT--ASDMLHMRWDELAFAKAYARQCVMGNKRGRR 85
QY 69 EENDVFSATLTNIPLEAGNSWSEIFELRGKYINKNGKTSINAM-----VMSHDK 121
DB 86 GENFATIDGMDVPL-AMEEMHNE-----REHYNLSAATGSPOMGCHTYVNAKTER 139
QY 122 LGCANVDCS-----GKTVY---VCOYGRPAKGGKTIYEKAPGSRSDGAGYTCDDDM 173
DB 140 IGCSSHCCEKLCGVETINELLYCNYEPGNVNGKRFQEGPSCQCP---SGYRC---- 192
QY 174 ONLGC 178
DB 193 KNSJC 197
```

```

RESULT 13
US-09-907-841-285
/ Sequence 285; Application US/09907841
/ Publication No. US20020198366A1
/ GENERAL INFORMATION:
/ APPLICANT: Genentech, Inc.
/ APPLICANT: Ashkenazi, Avi
/ APPLICANT: Botstein, David
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Eaton, Dan L.
/ APPLICANT: Ferrara, Napoleone
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gertschen, Mary E.
/ APPLICANT: Goddard, A.
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, Christopher J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth, J.
/ APPLICANT: Klievin, Ivar J.
/ APPLICANT: Mathier, Jennie P.
/ APPLICANT: Pan, James
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tunes, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William, I.
/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
/ FILE REFERENCE: 10466-14
/ CURRENT APPLICATION NUMBER: US/09/907,841
/ PRIOR APPLICATION NUMBER: PCT/US00/04414
/ PRIOR FILING DATE: 2001-11-20
/ PRIOR APPLICATION NUMBER: PCT/US00/04414
/ PRIOR FILING DATE: 2000-02-22
/ PRIOR APPLICATION NUMBER: US 60/143,048
/ PRIOR FILING DATE: 1999-07-07
/ PRIOR APPLICATION NUMBER: US 60/145,698
/ PRIOR FILING DATE: 1999-07-26
/ PRIOR APPLICATION NUMBER: US 60/146,222
/ PRIOR FILING DATE: 1999-07-28
/ PRIOR APPLICATION NUMBER: PCT/US99/20594
/ PRIOR FILING DATE: 1999-09-08
/ PRIOR APPLICATION NUMBER: PCT/US99/20944
/ PRIOR FILING DATE: 1999-09-13
/ PRIOR APPLICATION NUMBER: PCT/US99/21090
/ PRIOR FILING DATE: 1999-09-15
/ PRIOR APPLICATION NUMBER: PCT/US99/21547
/ PRIOR FILING DATE: 1999-09-15
/ PRIOR APPLICATION NUMBER: PCT/US99/23089
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: PCT/US99/28214
/ PRIOR FILING DATE: 1999-11-29
/ Remaining Prior Application data removed - See file wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 423
/ SEQ ID NO 285
/ LENGTH: 463
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-09-907-841-285

Query Match      15.9%; Score 159; DB 9; Length 463;
Best Local Similarity 28.6%; Pred. No. 1.2e-07;
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;

QY 13 LDDDMREMFELHNGRAAFARNTKTSKMTVYDCTLEKAYKSAKRC-----SEPPSSE 68
DB 28 LTDEKRLAYELHNLRYAQSPT--ASDMLHMRWDELAFAKAYARQCVMGNKRGRR 85
QY 69 EENDVFSATLTNIPLEAGNSWSEIFELRGKYINKNGKTSINAM-----VMSHDK 121
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; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089907
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089947
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090538
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07

Query Match      15.9%; Score 159; DB 9; Length 463;
Best Local Similarity 28.6%; Pred. No. 1.2e-07;
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;

OY      13 LDDDMREFTLHNGYRAAFARNYKTSKRTWYDCTLEEKAYKSAERC-----SEEPSSE 68
DB      28 LTDEERRLVVELHNLNYRAOVSP--ASDMLHRWDEELAAFAKAYAROCVWGHNRGR 85
OY      69 EENVDFSAATLNIPLDAGNSWSEIFELRGVYKNGKTSNIAM-----VYDSHDK 121
DB      86 GENLFAITDEGADVL-AMEEWHB-----REHYMLSATSPGOMCGHYTOVWAKTER 139
OY      122 LGCAYVDCS-----GKTHV---VCQYGPAAKDGKTIYEBGAPCSGSDYAGVTCDDDM 173
DB      140 IGGSHFCKLQGVHEITLVCNTEPEPNVKGKRPYQEGTPOSCP---SGYHC----- 192
OY      174 ONLJC 178
DB      193 KNSJC 197

RESULT 16
US-09-906-742-285
; Sequence 285; Application US/09906742
; Publication No. US20030023054A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Bostein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eason, Dan L
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvarin, Sherman
; APPLICANT: Fogel, Sherran
; APPLICANT: Geor, Wei-Olang
; APPLICANT: Gerlicsen, Mary E.
; APPLICANT: Goddard, A. Paul J.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimsaid, Christopher J.
; APPLICANT: Gunney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavir, Ivar J.
; APPLICANT: Mathier, Jenale P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumes, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
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; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,742
; CURRENT FILING DATE: 2001-07-15
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-06-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 285
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-906-742-285

Query Match      15.9%; Score 159; DB 9; Length 463;
Best Local Similarity 28.6%; Pred. No. 1.2e-07;
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;

OY      13 LDDDMREFTLHNGYRAAFARNYKTSKRTWYDCTLEEKAYKSAERC-----SEEPSSE 68
DB      28 LTDEERRLVVELHNLNYRAOVSP--ASDMLHRWDEELAAFAKAYAROCVWGHNRGR 85
OY      69 EENVDFSAATLNIPLDAGNSWSEIFELRGVYKNGKTSNIAM-----VYDSHDK 121
DB      86 GENLFAITDEGADVL-AMEEWHB-----REHYMLSATSPGOMCGHYTOVWAKTER 139
OY      122 LGCAYVDCS-----GKTHV---VCQYGPAAKDGKTIYEBGAPCSGSDYAGVTCDDDM 173
DB      140 IGGSHFCKLQGVHEITLVCNTEPEPNVKGKRPYQEGTPOSCP---SGYHC----- 192
OY      174 ONLJC 178
DB      193 KNSJC 197

RESULT 17
US-10-121-049-360
; Sequence 360; Application US/0121049
; Publication No. US20030022239A1
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GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William

US-10-123-904-360
Sequence 360, Application US/10123904
Publication No. US2003002238A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: Deforge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William

Query Match
Best Local Similarity 28.6%; Score 159; DB 9; Length 463;
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;

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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C54
CURRENT APPLICATION NUMBER: US/10/123,904
CURRENT FILING DATE: 2002-04-16
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 360
LENGTH: 463
TYPE: PRT
ORGANISM: Homo Sapien
US-10-123-904-360

Query Match
Best Local Similarity 28.6%; Score 159; DB 9; Length 463;
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;

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QY 13 LDDDMREMTLHNGYRAAFARNTKSKMTVYDCTLEKAKSAKNC-----SEEPSSE 68  
DB 28 LDEKRLMVLHMLHIAQVSP--ASDMLHMRWDELLAFAFAIAFROCVMGHKNGRR 85  
QY 69 BENVDYFSATLNTILEAGNSWSEIFELRGVYTKNGKTSNIANN-----VWDSHK 121  
DB 86 GENLFAITDEGMVPL-AMEEMHHE-----REHYNLSAATCSFGQCGHYTVVWAKTER 139  
QY 122 LCCAVVDCS-----GKTHV---VCQYGEAKDGKTYEAGAPCSKSDYAGVYCDDDW 173  
DB 140 ICGSHFCEKLGQVEETINELVNCNTEPPGNVKGKRPYOBETPCSOCP---SGYHC----- 192  
QY 174 QNTLC 178  
DB 193 KNSLC 197

RESULT 20  
US-09-906-838-285  
Sequence 285, Application US/09906838  
Publication No. US20030027145A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertschen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillen, Kenneth J.  
APPLICANT: Kijavita, Ivar J.  
APPLICANT: Mather, Jennie F.  
APPLICANT: Pan, James  
APPLICANT: Peoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
TITLE OF INVENTION: Acids and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/906, 838  
PRIOR FILING DATE: 2001-07-16  
PRIOR APPLICATION NUMBER: 09/665, 350  
PRIOR FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143, 048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145, 698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146, 222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 285  
LENGTH: 463  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-09-906-838-285

Query Match 15 9%: Score 159; DB 9; Length 463;  
Best Local Similarity 28 6%: Pred No 1, 2e-07;  
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;

QY 13 LDDDMREMTLHNGYRAAFARNTKSKMTVYDCTLEKAKSAKNC-----SEEPSSE 68  
DB 28 LDEKRLMVLHMLHIAQVSP--ASDMLHMRWDELLAFAFAIAFROCVMGHKNGRR 85  
QY 69 BENVDYFSATLNTILEAGNSWSEIFELRGVYTKNGKTSNIANN-----VWDSHK 121  
DB 86 GENLFAITDEGMVPL-AMEEMHHE-----REHYNLSAATCSFGQCGHYTVVWAKTER 139  
QY 122 LCCAVVDCS-----GKTHV---VCQYGEAKDGKTYEAGAPCSKSDYAGVYCDDDW 173  
DB 140 ICGSHFCEKLGQVEETINELVNCNTEPPGNVKGKRPYOBETPCSOCP---SGYHC----- 192  
QY 174 QNTLC 178  
DB 193 KNSLC 197

RESULT 21  
US-09-907-613-285  
Sequence 285, Application US/09907613  
Publication No. US20030027145A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gertschen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillen, Kenneth J.  
APPLICANT: Kijavita, Ivar J.  
APPLICANT: Mather, Jennie F.  
APPLICANT: Pan, James  
APPLICANT: Peoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey

```
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT FILING DATE: 2001-07-17
PRIORITY APPLICATION NUMBER: US/09/907,613
PRIORITY FILING DATE: 2000-02-22
PRIORITY APPLICATION NUMBER: PCT/US00/04414
PRIORITY FILING DATE: 1999-07-07
PRIORITY APPLICATION NUMBER: US 60/143,048
PRIORITY FILING DATE: 1999-07-07
PRIORITY APPLICATION NUMBER: US 60/145,698
PRIORITY FILING DATE: 1999-07-26
PRIORITY APPLICATION NUMBER: US 60/146,222
PRIORITY FILING DATE: 1999-07-28
PRIORITY APPLICATION NUMBER: PCT/US99/20594
PRIORITY FILING DATE: 1999-09-08
PRIORITY APPLICATION NUMBER: PCT/US99/20944
PRIORITY FILING DATE: 1999-09-13
PRIORITY APPLICATION NUMBER: PCT/US99/21090
PRIORITY FILING DATE: 1999-09-15
PRIORITY APPLICATION NUMBER: PCT/US99/21547
PRIORITY FILING DATE: 1999-09-15
PRIORITY APPLICATION NUMBER: PCT/US99/23089
PRIORITY FILING DATE: 1999-10-05
PRIORITY APPLICATION NUMBER: PCT/US99/28214
PRIORITY FILING DATE: 1999-11-29
PRIORITY APPLICATION NUMBER: PCT/US99/28313
PRIORITY FILING DATE: 1999-11-30
PRIORITY APPLICATION NUMBER: PCT/US99/28564
PRIORITY FILING DATE: 1999-12-02
PRIORITY APPLICATION NUMBER: PCT/US99/28565
PRIORITY FILING DATE: 1999-12-02
PRIORITY APPLICATION NUMBER: PCT/US99/30095
PRIORITY FILING DATE: 1999-12-16
PRIORITY APPLICATION NUMBER: PCT/US99/30911
PRIORITY FILING DATE: 1999-12-20
PRIORITY APPLICATION NUMBER: PCT/US99/30999
PRIORITY FILING DATE: 1999-12-20
PRIORITY APPLICATION NUMBER: PCT/US00/00219
PRIORITY FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 285
LENGTH: 463
TYPE: PRT
ORGANISM: Homo Sapien
US-09-907-613-285

Query Match      15.9%; Score 159; DB 9; Length 463;
Best Local Similarity 28.6%; Pred. No. 1.2e-07;
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;

OY 13 LDDNREMTLHNGYRAAFANNTYKTKMTWYDCTLEKAYKSAEC-----SEEPSSE 68
DB 28 LTDEKRLAYELNLRAQVST--ASDMLHMRDELAAFAKAYARQCWGHKRGRR 85
OY 69 EBNVDFSAATLNIPLEAGNSWSEITELGKYNNKNGTSTNIAM-----VMDSHDK 121
DB 86 GENFEATTDGMDVPL-ANEEWHNE-----REHYNLSAATYCSPGQMGCHYTOYVMAKTER 139
OY 122 LGCAVVDSC-----GKTHV---VCQYGPKEKGDGKTIYEGAPCSRSDYAGAGYTDGDM 173
DB 140 IGCSSHCCEELQCVETNIELVYCNYEPGNVAGKRPYDEGIPCSOCP---SGYHC----- 192
OY 174 ONLJC 178
DB 193 KNSJC 197

RESULT 22
US-09-907-942-285
; Sequence 285, Application US/09907942
; Publication No. US20030027146A1
; GENERAL INFORMATION:
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```
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Batton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherran
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kjaevn, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Peoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT FILING DATE: 2002-01-22
PRIORITY APPLICATION NUMBER: PCT/US00/04414
PRIORITY FILING DATE: 2000-02-22
PRIORITY APPLICATION NUMBER: US 60/143,048
PRIORITY FILING DATE: 1999-07-07
PRIORITY APPLICATION NUMBER: US 60/145,698
PRIORITY FILING DATE: 1999-07-26
PRIORITY APPLICATION NUMBER: PCT/US99/20594
PRIORITY FILING DATE: 1999-07-28
PRIORITY APPLICATION NUMBER: PCT/US99/20944
PRIORITY FILING DATE: 1999-09-13
PRIORITY APPLICATION NUMBER: PCT/US99/21090
PRIORITY FILING DATE: 1999-09-15
PRIORITY APPLICATION NUMBER: PCT/US99/21547
PRIORITY FILING DATE: 1999-09-15
PRIORITY APPLICATION NUMBER: PCT/US99/23089
PRIORITY FILING DATE: 1999-10-05
PRIORITY APPLICATION NUMBER: PCT/US99/28214
PRIORITY FILING DATE: 1999-11-29
PRIORITY APPLICATION NUMBER: PCT/US99/28313
PRIORITY FILING DATE: 1999-11-30
PRIORITY APPLICATION NUMBER: PCT/US99/28564
PRIORITY FILING DATE: 1999-12-02
PRIORITY APPLICATION NUMBER: PCT/US99/28565
PRIORITY FILING DATE: 1999-12-02
PRIORITY APPLICATION NUMBER: PCT/US99/30095
PRIORITY FILING DATE: 1999-12-16
PRIORITY APPLICATION NUMBER: PCT/US99/30911
PRIORITY FILING DATE: 1999-12-20
PRIORITY APPLICATION NUMBER: PCT/US99/30999
PRIORITY FILING DATE: 1999-12-20
PRIORITY APPLICATION NUMBER: PCT/US00/00219
PRIORITY FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 285
LENGTH: 463
TYPE: PRT
ORGANISM: Homo Sapien
US-09-907-942-285

Query Match      15.9%; Score 159; DB 9; Length 463;
Best Local Similarity 28.6%; Pred. No. 1.2e-07;
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Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;

Query 13 LDDMRKMTLHNGYRAAFARNTYTKMTWYDCTLEEKAYKAEK-----SEPSSE 68  
DB 28 LTDEKRLMVELHNLRYAOSPT--ASDMLHMRDELAFAKAYAROCVGNHKEGR 85  
DB 69 EENVDFSAATNIPLEAGNSWSEIFELRGKYNNKNGTSNANM-----VWDSHK 121  
DB 86 GENLFAITDEGMVPL-AMEEWHHE-----REHYNLSAATCSFGMCGHYTYVMKTER 139  
QY 122 LGCAVYDCS-----GKTHV---VCOYGEPAKDGKTIYEGAPCSRCSDYAGVTCDDM 173  
DB 140 ICGSHFCEKLOGVEETNIELLVYCNTEPBNVKNKRPYQEGTPCSQCP---SGYHC----- 192  
QY 174 ONLTC 178  
DB 193 KNSLC 197

RESULT 23  
US-10-175-746-360  
; Sequence 360, Application US/10175746  
; Publication No. US20030027270A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Flivaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Thomas, Daniel  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Collin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P330R1C353  
; CURRENT APPLICATION NUMBER: US/10/175,746  
; PRIOR APPLICATION: 2002-06-19  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 360  
; LENGTH: 463  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-175-746-360

Query Match 15.9%; Score 159; DB 9; Length 463;  
Best Local Similarity 28.6%; Pred. No. 1.2e-07;  
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;

RESULT 24  
US-10-176-918-360  
; Sequence 360, Application US/10176918  
; Publication No. US20030027275A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Flivaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Thomas, Daniel  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Collin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P330R1C382  
; CURRENT APPLICATION NUMBER: US/10/176,918  
; PRIOR APPLICATION: 2002-06-20  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 360  
; LENGTH: 463  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-176-918-360

Query Match 15.9%; Score 159; DB 9; Length 463;  
Best Local Similarity 28.6%; Pred. No. 1.2e-07;  
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;

QY 13 LDDMRKMTLHNGYRAAFARNTYTKMTWYDCTLEEKAYKAEK-----SEPSSE 68  
DB 28 LTDEKRLMVELHNLRYAOSPT--ASDMLHMRDELAFAKAYAROCVGNHKEGR 85  
QY 69 EENVDFSAATNIPLEAGNSWSEIFELRGKYNNKNGTSNANM-----VWDSHK 121  
DB 86 GENLFAITDEGMVPL-AMEEWHHE-----REHYNLSAATCSFGMCGHYTYVMKTER 139  
QY 122 LGCAVYDCS-----GKTHV---VCOYGEPAKDGKTIYEGAPCSRCSDYAGVTCDDM 173  
DB 140 ICGSHFCEKLOGVEETNIELLVYCNTEPBNVKNKRPYQEGTPCSQCP---SGYHC----- 192  
QY 174 ONLTC 178  
DB 193 KNSLC 197

RESULT 25  
US-10-176-921-360  
; Sequence 360, Application US/10176921  
; Publication No. US20030027276A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Flivaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.





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PRIORITY FILING DATE: 1999-07-07
PRIORITY APPLICATION NUMBER: US 60/145,698
PRIORITY FILING DATE: 1999-07-26
PRIORITY APPLICATION NUMBER: US 60/146,222
PRIORITY FILING DATE: 1999-07-28
PRIORITY APPLICATION NUMBER: PCT/US99/20594
PRIORITY FILING DATE: 1999-09-08
PRIORITY APPLICATION NUMBER: PCT/US99/20944
PRIORITY FILING DATE: 1999-09-13
PRIORITY APPLICATION NUMBER: PCT/US99/21090
PRIORITY FILING DATE: 1999-09-15
PRIORITY APPLICATION NUMBER: PCT/US99/21547
PRIORITY FILING DATE: 1999-09-15
PRIORITY APPLICATION NUMBER: PCT/US99/23089
PRIORITY FILING DATE: 1999-10-05
PRIORITY APPLICATION NUMBER: PCT/US99/28214
PRIORITY FILING DATE: 1999-11-29
PRIORITY APPLICATION NUMBER: PCT/US99/28313
PRIORITY FILING DATE: 1999-11-30
PRIORITY APPLICATION NUMBER: PCT/US99/28564
PRIORITY FILING DATE: 1999-12-02
PRIORITY APPLICATION NUMBER: PCT/US99/28565
PRIORITY FILING DATE: 1999-12-02
PRIORITY APPLICATION NUMBER: PCT/US99/30095
PRIORITY FILING DATE: 1999-12-16
PRIORITY APPLICATION NUMBER: PCT/US99/30911
PRIORITY FILING DATE: 1999-12-20
PRIORITY APPLICATION NUMBER: PCT/US99/30999
PRIORITY FILING DATE: 1999-12-20
PRIORITY APPLICATION NUMBER: PCT/US00/00219
PRIORITY FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 285
TYPE: PRT
LENGTH: 463
ORGANISM: Homo Sapien
US-09-904-859-285
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Query Match 15.9% Score 159; DB 9; Length 463;
Best Local Similarity 28.6% Pred. No. 1.2e-07;
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;
```

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QY 13 LDDMRKMTFELHNGRAAFARNTKTSKMTVYDCTLEKAYSAEC-----SEEPSSE 68
DB 28 LTDEKRLMVELHNLRAQVSP--ASDMLHMRWDEELAAFAKAYAROCVGHKRGRR 85
QY 69 EENVDFSAATLNIPLEAGNSWMSSEIFELRGKYNNKNGTSNIANN-----VMDSHDK 121
DB 86 GENLFAITDEGMDVPL-AMEEMHNE-----REHYNLSAATCSPGOMCGHYTOVVMATKTER 139
QY 122 LGCAVWDCS-----GRTYV--VCQYGPFAKGDGKTIIEEGAPCSRSDGAGVTCDDDW 173
DB 140 IGCSEHCEKLOGVEETNIELVCNYPEPQNVKGRKPYOEGTSCQCP--SGYHC----- 192
QY 174 ONLJC 178
DB 193 KNSJC 197
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RESULT 30
US-09-909-204-285
Sequence 285; Application US/09909204
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botschein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
```

```

APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT FILING DATE: 2001-07-18
PRIORITY FILING DATE: 2000-02-22
PRIORITY APPLICATION NUMBER: PCT/US00/04414
PRIORITY FILING DATE: 1999-07-07
PRIORITY APPLICATION NUMBER: US 60/145,698
PRIORITY FILING DATE: 1999-07-26
PRIORITY APPLICATION NUMBER: US 60/146,222
PRIORITY FILING DATE: 1999-07-28
PRIORITY APPLICATION NUMBER: PCT/US99/20594
PRIORITY FILING DATE: 1999-09-08
PRIORITY APPLICATION NUMBER: PCT/US99/20944
PRIORITY FILING DATE: 1999-09-13
PRIORITY APPLICATION NUMBER: PCT/US99/21090
PRIORITY FILING DATE: 1999-09-15
PRIORITY APPLICATION NUMBER: PCT/US99/21547
PRIORITY FILING DATE: 1999-09-15
PRIORITY APPLICATION NUMBER: PCT/US99/23089
PRIORITY FILING DATE: 1999-10-05
PRIORITY APPLICATION NUMBER: PCT/US99/28214
PRIORITY FILING DATE: 1999-11-29
PRIORITY APPLICATION NUMBER: PCT/US99/28313
PRIORITY FILING DATE: 1999-11-30
PRIORITY APPLICATION NUMBER: PCT/US99/28564
PRIORITY FILING DATE: 1999-12-02
PRIORITY APPLICATION NUMBER: PCT/US99/28565
PRIORITY FILING DATE: 1999-12-02
PRIORITY APPLICATION NUMBER: PCT/US99/30095
PRIORITY FILING DATE: 1999-12-16
PRIORITY APPLICATION NUMBER: PCT/US99/30911
PRIORITY FILING DATE: 1999-12-20
PRIORITY APPLICATION NUMBER: PCT/US99/30999
PRIORITY FILING DATE: 1999-12-20
PRIORITY APPLICATION NUMBER: PCT/US00/00219
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 285
TYPE: PRT
LENGTH: 463
ORGANISM: Homo Sapien
US-09-909-204-285
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Query Match 15.9% Score 159; DB 9; Length 463;
Best Local Similarity 28.6% Pred. No. 1.2e-07;
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;
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QY 13 LDDMRKMTFELHNGRAAFARNTKTSKMTVYDCTLEKAYSAEC-----SEEPSSE 68
DB 28 LTDEKRLMVELHNLRAQVSP--ASDMLHMRWDEELAAFAKAYAROCVGHKRGRR 85
QY 69 EENVDFSAATLNIPLEAGNSWMSSEIFELRGKYNNKNGTSNIANN-----VMDSHDK 121
DB 86 GENLFAITDEGMDVPL-AMEEMHNE-----REHYNLSAATCSPGOMCGHYTOVVMATKTER 139
```







APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlitsen, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kilevlo, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/906,700  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21090  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095  
PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
PRIOR FILING DATE: 2000-01-05  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 285  
LENGTH: 463  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-09-906-700-285

Query Match 15.9%; Score 159; DB 9; Length 463;  
Best Local Similarity 28.6%; Pred. No. 1.2e-07;  
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;

QY 13 LDDDMKEMTELHNGYRAAFARNYTKSMRTMYDCTLEEKAKYSAEC-----SEPPSS 68

DB 28 LTDEERKLAVELHNIYRAOVSPT--ASDMLHRMDEELAAFAAAYAROCVWGHNRERR 85  
QY 69 EENVDFSAATLNIPILEGNSMWSSEIFELRGVYKKNKTSNIANN-----VWDSHK 121  
DB 86 GENLFAITDEGADYPL-AMEBWHB-----REHYNLSAATCSPGOCGHYTOYVAKTER 139  
QY 122 LGCAYVDCS-----GKTHV---VCOTGPEAKGDKTIYEBGAPCSRCSDYGAGVTCDDDW 173  
DB 140 ICGSHFECKLOGVEETNIELVLCNTEPRGNVKGKRPYOBGTPOSCP---SGYHC----- 192  
QY 174 ONLNC 178  
DB 193 KNSLC 197

RESULT 36  
US-10-140-002-360  
Sequence 360, Application US/10140002  
Publication No. US20030037623A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerlitsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3330R1C59  
CURRENT APPLICATION NUMBER: US/10/140,002  
CURRENT FILING DATE: 2002-05-06  
Prior Application removed - See Palm or File Wrapper  
NUMBER OF SEQ ID NOS: 550  
SEQ ID NO 360  
LENGTH: 463  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-140-002-360

Query Match 15.9%; Score 159; DB 9; Length 463;  
Best Local Similarity 28.6%; Pred. No. 1.2e-07;  
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;

QY 13 LDDDMKEMTELHNGYRAAFARNYTKSMRTMYDCTLEEKAKYSAEC-----SEPPSS 68  
DB 28 LTDEERKLAVELHNIYRAOVSPT--ASDMLHRMDEELAAFAAAYAROCVWGHNRERR 85  
QY 69 EENVDFSAATLNIPILEGNSMWSSEIFELRGVYKKNKTSNIANN-----VWDSHK 121  
DB 86 GENLFAITDEGADYPL-AMEBWHB-----REHYNLSAATCSPGOCGHYTOYVAKTER 139  
QY 122 LGCAYVDCS-----GKTHV---VCOTGPEAKGDKTIYEBGAPCSRCSDYGAGVTCDDDW 173  
DB 140 ICGSHFECKLOGVEETNIELVLCNTEPRGNVKGKRPYOBGTPOSCP---SGYHC----- 192  
QY 174 ONLNC 178  
DB 193 KNSLC 197

RESULT 37

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US-09-902-903-285
Sequence 285, Application US/09092903
Publication No. US20030044839A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gierlsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Paoni, Nicholas P.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,903
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 285
LENGTH: 463
TYPE: PRT
ORGANISM: Homo Sapien

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US-09-902-903-285
Query Match 15.9% Score 159; DB 9; Length 463;
Best Local Similarity 28.6% Pred. No. 1,2e-07;
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9

OY 13 LDDMHEMTLHNGYAAAFANRYTSTKMTMYDCTLEKAYSAENK---SPESSSE 68
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 28 LTDEERKLWELHMLHLYIAOVSFP--ASDMLHMHMDDELAAAKAYIAOCYMGHNENGR 85
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 69 EENVYVESATLNIPLPDEAGNSWSETEFLKGYTKNKGKTSYINAM-----VYDSHK 121
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 86 GENLFATIDEGADVPL-AMEEWNHE-----REYHLSAATSPSPQCMGHYTOYWATER 139
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 122 LGCAYVYDCS-----GKTHV---VCQYGEPAKGDGKITYEBCAPCSRSDYAGYTCDDW 173
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 140 ICGSHFECKKLGQVEETINELLVCHTEPPEGNVKGKHPYQECTPSOCF---SGYHC---- 192
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 174 QNTLC 178
      | | |
DB 193 KNSLC 197

RESULT 38
US-09-903-749A-285
Sequence 285, Application US/09903749A
Publication No. US20030045693A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fillyaroff, Ellen
APPLICANT: Fogel, Sherman
APPLICANT: Geor, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertelsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Mathier, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoul, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/903,749A
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547

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Tue Jul 15 09:48:47 2003

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Page 21

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PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 285
LENGTH: 463
TYPE: PRT
ORGANISM: Homo Sapien
US-09-903-749A-285

Query Match      15.9%  Score 159; DB 9; Length 463;
Best Local Similarity 28.6%; Pred. No. 1.2e-07; Indels 34; Gaps 9;
Matches 53; Conservative 72; Mismatches 72;

QY 13 LDDMKREMTLHNGYRAAFARNTSKRTVYDCTLEEKAVKSAEKC-----SEEPSE 68
DB 28 LTDEERKLAVELHNLNRYKQVSP--ASDMLHMRWDELAFAKRYAROCVGMHNKERRR 85
QY 69 EENVDFSAATINILPELAGNSWSEIFELRGVYKKNKSTNINM-----VWDSHK 121
DB 86 GENLFAITDEGMDVPL-AMEEMHNE-----REHYNLSAATCSPGOMCGHYTVVAKTER 139
QY 122 ICGCAVVDGS-----GKTHV---VCOYGPFAKGDGTIEEGAPCSRSDYGAVTCDDDW 173
DB 140 ICGGSHRCKEIGVETNIELVLCNYPEPQVNGKRPYQEGTSCOP--SGYHC----- 192
QY 174 ONLIC 178
DB 193 KNSLC 197

RESULT 39
US-09-903-786-285
Sequence 285 Application US/09903786
Publication No. US20030044793A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Flieraroff, Ellen
APPLICANT: Food, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertelsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Peoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
```

```

APPLICANT: Stewart, Timothy A.
APPLICANT: Nunes, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William J.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US/09/903,786
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 285
LENGTH: 463
TYPE: PRT
ORGANISM: Homo Sapien
US-09-903-786-285

Query Match      15.9%  Score 159; DB 9; Length 463;
Best Local Similarity 28.6%; Pred. No. 1.2e-07; Indels 34; Gaps 9;
Matches 53; Conservative 72; Mismatches 72;

QY 13 LDDMKREMTLHNGYRAAFARNTSKRTVYDCTLEEKAVKSAEKC-----SEEPSE 68
DB 28 LTDEERKLAVELHNLNRYKQVSP--ASDMLHMRWDELAFAKRYAROCVGMHNKERRR 85
QY 69 EENVDFSAATINILPELAGNSWSEIFELRGVYKKNKSTNINM-----VWDSHK 121
DB 86 GENLFAITDEGMDVPL-AMEEMHNE-----REHYNLSAATCSPGOMCGHYTVVAKTER 139
QY 122 ICGCAVVDGS-----GKTHV---VCOYGPFAKGDGTIEEGAPCSRSDYGAVTCDDDW 173
DB 140 ICGGSHRCKEIGVETNIELVLCNYPEPQVNGKRPYQEGTSCOP--SGYHC----- 192
QY 174 ONLIC 178
DB 193 KNSLC 197
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RESULT 40  
US-10-142-419-360  
Sequence 360, Application US/10142419  
Publication No. US20030044945A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: DeForge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Fillardoff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
FILE REFERENCE: P3330R1C244  
CURRENT APPLICATION NUMBER: US/10/142,419  
CURRENT FILING DATE: 2002-05-10  
Prior Application removed - See File Wrapper or Palm  
SEQ ID NO 360  
LENGTH: 463  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-142-419-360  
Query Match 15.9%; Score 159; DB 9; Length 463;  
Best Local Similarity 28.6%; Pred. No. 1.2e-07;  
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;  
DB 13 LDDMRKEMFTELHNGRAAFARNYTSKARTWYDCTLEBKAYKSAEC-----SEPPSE 68  
DB 28 LTDEERKLWELHNLHRAOVSP--ASDMLHMRWDELAFAKAYAROCVGNHKKERR 85  
QY 69 EENVDFSAATLNIPLDGNMWSSEIFELRGKYNNKNGKTSNIANN-----VMDSHDK 121  
DB 86 GENLFAITDEGMVPL-AMEEWNHE-----REHYNLSAATCSPGOMCGHYTVVMAKTER 139  
QY 122 LGCAYVDCS-----GKTHV--VCOYGPPEAKGKGKTIIEBAPCSRSDYAGAYCDDDW 173  
DB 140 ICGSHFCKLQGVETNIETLVCAVTEPPGNVKKRPFQESTPCSCP---SGYHC----- 192  
QY 174 ONLIG 178  
DB 193 KNSLC 197  
RESULT 41  
US-09-902-736-285  
Sequence 285, Application US/09902736  
Publication No. US20030049676A1  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fillardoff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlitsen, Mary E.  
APPLICANT: Goddard, A.

APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth, J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paonli, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William, I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/902,736  
CURRENT FILING DATE: 2001-07-10  
Prior Application Number: 09/665,350  
Prior Filing Date: 2000-09-18  
Prior Application Number: PCT/US00/04414  
Prior Filing Date: 2000-02-22  
Prior Application Number: US 60/143,048  
Prior Filing Date: 1999-07-28  
Prior Application Number: US 60/146,222  
Prior Filing Date: 1999-07-28  
Prior Application Number: PCT/US99/20594  
Prior Filing Date: 1999-09-08  
Prior Application Number: PCT/US99/20944  
Prior Filing Date: 1999-09-13  
Prior Application Number: PCT/US99/21090  
Prior Filing Date: 1999-09-15  
Prior Application Number: PCT/US99/21547  
Prior Filing Date: 1999-09-15  
Prior Application Number: PCT/US99/23089  
Prior Filing Date: 1999-10-05  
Prior Application Number: PCT/US99/28214  
Prior Filing Date: 1999-11-29  
Prior Application Number: PCT/US99/28313  
Prior Filing Date: 1999-11-30  
Prior Application Number: PCT/US99/28564  
Prior Filing Date: 1999-12-02  
Prior Application Number: PCT/US99/28565  
Prior Filing Date: 1999-12-02  
Prior Application Number: PCT/US99/30095  
Prior Filing Date: 1999-12-16  
Prior Application Number: PCT/US99/30911  
Prior Filing Date: 1999-12-20  
Prior Application Number: PCT/US99/30999  
Prior Filing Date: 1999-12-20  
Prior Application Number: PCT/US00/00219  
Prior Filing Date: 2000-01-05  
SEQ ID NO 285  
LENGTH: 463  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-09-902-736-285  
Query Match 15.9%; Score 159; DB 9; Length 463;  
Best Local Similarity 28.6%; Pred. No. 1.2e-07;  
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;  
DB 13 LDDMRKEMFTELHNGRAAFARNYTSKARTWYDCTLEBKAYKSAEC-----SEPPSE 68  
DB 28 LTDEERKLWELHNLHRAOVSP--ASDMLHMRWDELAFAKAYAROCVGNHKKERR 85  
QY 69 EENVDFSAATLNIPLDGNMWSSEIFELRGKYNNKNGKTSNIANN-----VMDSHDK 121  
DB 86 GENLFAITDEGMVPL-AMEEWNHE-----REHYNLSAATCSPGOMCGHYTVVMAKTER 139

OY 122 LGCAYVDCS-----GKTHV---VCQYGPBANGDKTIYEBGAFCSKSDYAGAYTCDDM 173  
DB 140 ICGSHFEKLOGVEETINIELVNCNTEPBNVKNRPPYQGTSCCP---SGYHC----- 192  
OY 174 ONLJC 178  
DB 193 KNSLC 197

RESULT 42  
US-09-904-119-285  
Sequence 285, Application US/09904119  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gersten, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillen, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/904,119  
PRIOR FILING DATE: 2001-07-11  
PRIOR APPLICATION NUMBER: 09/655,350  
PRIOR FILING DATE: 2000-09-18  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048  
PRIOR FILING DATE: 1999-07-07  
PRIOR APPLICATION NUMBER: US 60/145,698  
PRIOR FILING DATE: 1999-07-26  
PRIOR APPLICATION NUMBER: US 60/146,222  
PRIOR FILING DATE: 1999-07-28  
PRIOR APPLICATION NUMBER: PCT/US99/20594  
PRIOR FILING DATE: 1999-09-08  
PRIOR APPLICATION NUMBER: PCT/US99/20944  
PRIOR FILING DATE: 1999-09-13  
PRIOR APPLICATION NUMBER: PCT/US99/21050  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/21547  
PRIOR FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: PCT/US99/23089  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: PCT/US99/28214  
PRIOR FILING DATE: 1999-11-29  
PRIOR APPLICATION NUMBER: PCT/US99/28313  
PRIOR FILING DATE: 1999-11-30  
PRIOR APPLICATION NUMBER: PCT/US99/28564  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/28565  
PRIOR FILING DATE: 1999-12-02  
PRIOR APPLICATION NUMBER: PCT/US99/30095

PRIOR FILING DATE: 1999-12-16  
PRIOR APPLICATION NUMBER: PCT/US99/30911  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US99/30999  
PRIOR FILING DATE: 1999-12-20  
PRIOR APPLICATION NUMBER: PCT/US00/00219  
NUMBER OF SEQ ID NOS: 423  
SEQ ID NO 285  
LENGTH: 463  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-09-904-119-285

Query Match 15.9%; Score 159; DB 9; Length 463;  
Best Local Similarity 28.6%; Pred. No. 1,2e-07;  
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;

OY 13 LDDMREMTLHNGRYRAFAFRNKTYSKMTWYDCTLEKAYSAEK-----SEPPSSE 68  
DB 28 LTDEKRLWEHLNIXRQVPT--ASDMLHRMDELAARAKAYACQVGNKRRGR 85  
OY 69 EENVDFSAATINIELENGNSWSEIFELRGKYRNKNGTINIAM-----YNDSHDK 121  
DB 86 GENFALIDGKHVFL-AMERHHE-----RETNLSATSCSPQMGCHITVOYAKTER 139  
OY 122 LGCAYVDCS-----GKTHV---VCQYGPBANGDKTIYEBGAPCSKSDYAGAYTCDDM 173  
DB 140 ICGSHFEKLOGVEETINIELVNCNTEPBNVKNRPPYQGTSCCP---SGYHC----- 192  
OY 174 ONLJC 178  
DB 193 KNSLC 197

RESULT 43  
US-09-904-956-285  
Sequence 285, Application US/09904956  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gersten, Mary E.  
APPLICANT: Goddard, A.  
APPLICANT: Grimaldi, Christopher J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillen, Kenneth J.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Mather, Jennie P.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: 10466-14  
CURRENT APPLICATION NUMBER: US/09/904,956  
PRIOR FILING DATE: 2001-07-12  
PRIOR APPLICATION NUMBER: PCT/US00/04414  
PRIOR FILING DATE: 2000-02-22  
PRIOR APPLICATION NUMBER: US 60/143,048

```

PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 285
LENGTH: 463
TYPE: PRT
ORGANISM: Homo Sapien
US-09-904-956-285

Query Match      15.9%: Score 159; DB 9; Length 463;
Best Local Similarity 28.6%; Pred. No. 1.2e-07;
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;

QY 13 LDDMRKMTFLHNGVRAAFARNTKSKRTMYDCTLEKAYKSAEC-----SEPPSS 68
DB 28 LTDERKRLMVELHNLIRAOVSPT--ASDMLHMRDEELAFKAYAROCVGNHKEGR 85
QY 69 EENVDFSAATLNIPLKAGNSMSEIFELRGKYTNKNGKTSNIANN-----VMDSHK 121
DB 86 GENLEAITDEGMDVPL-AEEMHHE-----REHYNLISATSCSPQOMCGHYTQVYAKTER 139
QY 122 LGCAVVDSCS-----GKTHV---VCQYSPKAGDKITTEGAPCSRSDYAGAVTCDDM 173
DB 140 IGCSEHCEKLGVEETINELLYCNYPGNVYKGRNPVOEGTSCOP---SGYHC----- 192
QY 174 QNLIC 178
DB 193 KNSLIC 197

RESULT 44
US-09-907-794-285
; Sequence 285, Application US/09907794
; Publication No. US2003004967A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Geo, Wei-Qiang

```

```

APPLICANT: Gerber, Hanspeter
APPLICANT: Gertsen, Mary E.
APPLICANT: Goddard, A. Paul J.
APPLICANT: Godwaski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kjaer, Jennie P.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: US/09/907,794
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 285
LENGTH: 463
TYPE: PRT
ORGANISM: Homo Sapien
US-09-907-794-285

Query Match      15.9%: Score 159; DB 9; Length 463;
Best Local Similarity 28.6%; Pred. No. 1.2e-07;
Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;

QY 13 LDDMRKMTFLHNGVRAAFARNTKSKRTMYDCTLEKAYKSAEC-----SEPPSS 68
DB 28 LTDERKRLMVELHNLIRAOVSPT--ASDMLHMRDEELAFKAYAROCVGNHKEGR 85
QY 69 EENVDFSAATLNIPLKAGNSMSEIFELRGKYTNKNGKTSNIANN-----VMDSHK 121

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Db      86 GENTRALIDEGMDVPL-AMEEMHNE-----REHYNLSTATCSPOGKCGHYTYVWAKTER 139
OY      122 LGCAYVDCS-----GKTHV---VCQYGPBAGKDGKTIYEGAPCSRSDYGAGVTCDDW 173
Db      140 ICGSHFCEKIQVEETIELLVCNTEPPGNVKGKRPYOGTPTCSQCP-----SGYHC----- 192
OY      174 QNLIC 178
Db      193 KNSLC 197
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## RESULT 45

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US-10-123-262-360
: Sequence 360, Application US/10123262
: Publication No. US20030049816A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Beresini, Maureen
: APPLICANT: DeForge, Laura
: APPLICANT: Desnoyers, Luc
: APPLICANT: Filvarioff, Ellen
: APPLICANT: Gao, Wei-Qiang
: APPLICANT: Gerlsten, Mary E.
: APPLICANT: Goddard, Audrey J.
: APPLICANT: Godowski, Paul J.
: APPLICANT: Guiney, Austin L.
: APPLICANT: Sherwood, Steven
: APPLICANT: Smith, Victoria
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Wetanabe, Colin K
: APPLICANT: Wood, William
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P3330R1C38
: CURRENT APPLICATION NUMBER: US/10/123,262
: PRIOR APPLICATION DATE: 2002-04-15
: PRIOR APPLICATION REMOVED - See File Wrapper or Palm
: NUMBER OF SEQ ID NOS: 550
: SEQ ID NO 360
: LENGTH: 463
: TYPE: PRT
: ORGANISM: Homo Sapien
US-10-123-262-360
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Query Match      15.98; Score 159; DB 9; Length 463;
Best Local Similarity 28.68; Pred No. 1.2e-07;
Matches 53; Conservative 72; Mismatches 72; Indels 34; Gaps 9;
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OY      13 LDDDBREMFELHNGYRAAFARNYKTSKRPVYDCTLEKAYKSAEC-----SEPSSE 68
Db      28 LIDDERKRLMVLNHLRYAOVSPT--ASDHLHRNDEELAFKAYARQCVMGHNKNGRR 85
OY      69 EENVDFSAATLNIPLAGNSWSEFELRGVYNKNGKTSNIAM-----VYDSHDK 121
Db      86 GENTRALIDEGMDVPL-AMEEMHNE-----REHYNLSTATCSPOGKCGHYTYVWAKTER 139
OY      122 LGCAYVDCS-----GKTHV---VCQYGPBAGKDGKTIYEGAPCSRSDYGAGVTCDDW 173
Db      140 ICGSHFCEKIQVEETIELLVCNTEPPGNVKGKRPYOGTPTCSQCP-----SGYHC----- 192
OY      174 QNLIC 178
Db      193 KNSLC 197
```

Search completed: July 15, 2003, 08:37:15  
Job time : 26 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 15, 2003, 08:32:08 ; Search time 40 Seconds  
(without alignments)

435,008 Million cell updates/sec

Title: US-09-937-555a-2

Sequence: 1 EGDYSLCQCRKLEDDDDMM.....DYAGVTCDDDDMQLTIGH 181

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database: PIR.73.\*

1: Clr1.\*  
2: Plr2.\*  
3: Plr3.\*  
4: Plr4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	290	29.1	274	2	A54419
2	209.5	21.0	246	2	T24493
3	190	19.1	425	2	C89753
4	154.5	15.5	207	2	T22436
5	153	15.3	213	2	T22439
6	152	15.2	212	2	T22437
7	146.5	14.7	208	2	T19852
8	143	14.3	207	2	T22438
9	142	14.2	210	2	T19849
10	140.5	14.1	211	2	T19859
11	139	13.9	262	2	T24854
12	138.5	13.9	209	2	T19848
13	137.5	13.8	209	2	T19847
14	137	13.7	243	2	B33329
15	133.5	13.4	207	2	T22432
16	132	13.2	245	2	A33329
17	127	12.7	243	2	A33329
18	124	12.4	196	2	T27833
19	122	12.2	266	2	Jc5308
20	121.5	12.2	208	2	T20651
21	121	12.1	207	2	T31959
22	121	12.1	219	2	Jc4131
23	121	12.1	243	2	Jc5020
24	119.5	12.0	244	2	A52902
25	118	11.8	161	2	T23299
26	118	11.8	283	2	DB6143
27	113	11.3	263	2	T04969
28	112.5	11.3	227	2	A11085
29	112.5	11.3	385	2	T21763

30	112	11.2	204	2	B44583	venom allergen ant
31	111.5	11.2	202	2	B44583	venom allergen ant
32	110.5	11.1	206	2	B44583	venom allergen ant
33	110	11.0	213	2	B31085	antigen 5-3-precu
34	108.5	10.9	205	2	D44583	venom allergen ant
35	108.5	10.9	212	2	B27834	hypothetical prote
36	107	10.7	204	2	B37339	antigen 5-3-precu
37	107	10.7	212	2	B27834	hypothetical prote
38	106	10.6	204	2	B44583	venom allergen ant
39	105.5	10.6	202	2	B44583	venom allergen ant
40	105	10.5	208	2	B29676	hypothetical prote
41	105	10.5	241	2	B33397	hypothetical prote
42	105	10.5	212	2	B44583	hypothetical prote
43	103	10.3	204	2	B44583	venom allergen ant
44	103	10.3	212	2	B44583	venom allergen ant
45	101	10.1	212	2	B57350	hypothetical prote

## ALIGNMENTS

RESULT 1  
A54419  
neutrophil inhibitory factor precursor - Ancylostoma caninum  
C/Species: Ancylostoma caninum  
C/Date: 19-Mar-1997 #sequence-revision 19-Mar-1997 #text-change 05-Nov-1999  
C/Accession: A54419  
R/Moyle, M.; Foster, D.L.; McGrath, D.E.; Brown, S.M.; Laroche, Y.; De Meuter, J.;  
J. Biol. Chem. 269, 10008-10015, 1994  
A/Title: A hookworm glycoprotein that inhibits neutrophil function is a ligand of t  
A/Reference number: A54419; MUID:94193581; PMID:7908286  
A/Accession: A54419  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-274 <MOY>  
A/Cross-references: GB:I27427; NID:g440279; PIDN:AAA27789.1; PID:g440280

Query Match 29.1%, Score 290; DB 2; Length 274;  
Best Local Similarity 34.3%; Pred. No. 1.7e-18;

Matches 69; Conservative 23; Mismatches 57; Indels 52; Gaps 7;

QY	14	DDDMREMETELHNGYRAAFARNY-----KTSKMTMYDCTL 50
DB	35	NDISIRLQFLAHMNGYRSKALGHISTEESDDDDDFGLPFPARAKMYLTDDEA 94
QY	51	EERAYKSAEKSE--PSEENVDVFSAATLNI---PLEAGNSWSEIFPL-----R 98
DB	95	EKAYVMSARNCSDSSPPEEDYDKNTKIFENSV-NISEALKAMISAKAFYLNKTRGE 153
QY	99	GKRYNKGKTSNINAMVDSHDKLCAYDC-----SGKT-----HYVCQYQPE 142
DB	154	GVLYSNHDISFANLAWDAKREKGVVNCPLGEIDETNHDGTYATTIVVCHPKI 213
QY	143	AKGDGKTIYEGACRCSYD 163
DB	214	NKTEGQPIKVTGTPDCDSRY 234

## RESULT 2

T24493  
hypothetical protein T05A10.5 - Caenorhabditis elegans  
C/Species: Caenorhabditis elegans  
C/Date: 15-Oct-1999 #sequence-revision 15-Oct-1999 #text-change 17-Mar-2000  
C/Accession: T24493  
R/Sulston, J.  
submitted to the EMBL Data Library, November 1995  
A/Reference number: Z19898  
A/Accession: T24493  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-246 <MIL>  
A/Cross-references: EMBL:Z68108; PIDN:CAA92136.1; GSPDB:GNO0028; CESP:T05A10.5  
A/Experimental source: clone T05A10



C:Genetics:  
A:Gene: CESP:T05A10.5  
A:Map position: X  
A:Introns: 66/2; 142/3; 179/3; 208/2  
C:Superfamily: cysteine-rich secretory protein 1

Query Match 21.0%; Score 209.5; DB 2; Length 246;  
Best Local Similarity 27.2%; Pred. No. 2.4e-11;  
Matches 59; Conservative 26; Mismatches 87; Indels 45; Gaps 7;

QY 6 LCOGKREKDD-----MKEMTELHNGYRAAFARVY-----KTSK 40  
DB 29 LCOAPSMVYKDGSGFQCNLSVSDVTRNFTLRQHNFYSRLAKGFENNGETNTSQPKASQ 88  
QY 41 MRTWYDCTLEERAKYSAKSC-----SEEPSSEENVDFSAAT---LNIPLEAGNSMW 91  
DB 89 MIKERYDCKMLERFAQNMAMNCVFAHSAHYERPNOGNTLMSFSPNDPRSLHTHTAEKMW 148  
QY 92 SEIFE-----LNGKYNNKNGKT-SNIANNVMSHDKLCAVVDGSGKTHVCOYGP 142  
DB 149 QELEERETPIDNVLPFELMDLKRAIGHYQAMDRTRLCGIANGPKMSYVYCHYGA 208  
QY 143 AKGDGKTYEEGAPCSRSDYGAGVTCDDDMQMLCI 179  
DB 209 GNRKNKTYEIGDDPCEVDDCPICTDCK--TTSICLV 243

RESULT 3  
C89753  
protein F11C7.3 (imported) - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Nov-2001  
C:Accession: C89753  
R:nonomys, The C. elegans Sequencing Consortium.  
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog  
A:Reference number: A75000; WUID:99069613; PMID:9851916  
A:Note: see websites genome.wustl.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C\_ele  
A:Accession: C89753  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1925 <STRO>  
A:Cross-references: GB:chr\_X; PIDN:MAC69015.1; PID:g29141420; GSPDB:GN00028; CESP:F11C7.3  
A:Gene: F11C7.3  
A:Map position: X

Query Match 19.1%; Score 190; DB 2; Length 425;  
Best Local Similarity 23.0%; Pred. No. 2.6e-09;  
Matches 45; Conservative 40; Mismatches 79; Indels 32; Gaps 5;

QY 4 YSLCQQRERLDDMEFTELHNGYRAAFARVYKTSK-----RTMYDCTL 50  
DB 222 FTMCPVTVDOQAQONFLDTHNKLRTSLAKGLADGIAAGAFAPMAKOMPKLVKYSCTV 281  
QY 51 EERAKYSAKSCSEEPSSE-----NDVFSATLNIPL-----BAGSNMSEIFE----- 96  
DB 282 EANNARTWAGCLYOHSTSAQRPGAGENTLYMISNNPKIOTRAEDSSKAMWSEIKDFGVS 341  
QY 97 ---LRGVYNNKNGKTSNIANNVMSHDKLCAVVDGSGKTHVCOYGPPEAKGDKGKTYEE 153  
DB 342 DNILTOAVFDRG--VGHTQAMAGETGICFEVENCFFETYSVCOYPAQNNYNNOLITRK 399  
QY 154 GAPCSRSDYGAGVTC 169  
DB 400 GSPCTADADCPGTCTC 415

RESULT 4  
T22436  
hypothetical protein F49E11.9 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 21-Jan-2000  
C:Accession: T22436  
R:Baynes, C.  
submitted to the EMBL Data Library, March 1996  
A:Reference number: T22436  
A:Accession: T22436  
A:Status: preliminary; translated from GB/EMBL/DDB  
A:Molecule type: DNA  
A:Residues: 1-207 <WII>  
A:Cross-references: EMBL:T20308; PIDN:CAA94348.1; GSPDB:GN00022; CESP:F49E11.9  
A:Experimental source: clone F49E11  
C:Genetics:  
A:Map position: 4  
A:Introns: 56/3; 102/3; 175/2  
C:Superfamily: yellowjacket venom allergen 5

Query Match 15.5%; Score 154.5; DB 2; Length 207;  
Best Local Similarity 26.6%; Pred. No. 1.6e-06;  
Matches 49; Conservative 19; Mismatches 71; Indels 45; Gaps 7;

QY 23 ELHNGYRAAFARVYKTSK-----MRTWYDCTLEERAKYSAKSCSEEPSSE--- 70  
DB 26 DAHNLRSAIAKSTYVAKGTKEPATDKRKVYDSVYAAAGNTANTC---PTGHSKGTG 82  
QY 71 -----NDVFSATLNIPLBAGSNMSEIFEELRKVYK-----NGKTSNIANN 114  
DB 83 YGENLYMSWTSAADVGSIDSYG---EIAAAWEKEFDGFKSNAMDITLFGSIGGATG 139  
QY 115 VVDSHDKLCAVVDGSG-----GKTHVCOYGPPEAKGDKTYEEKAPCSRSDYGAG 166  
DB 140 ANAANTSIGCVYKNGDMSNMNMKIVCOYSPQNTMGRPIIKETTSKSS---GS 196  
QY 167 VVCD 170  
DB 197 TKCD 200

RESULT 5  
T22439  
hypothetical protein F49E11.4 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
C:Accession: T22439  
R:Baynes, C.  
submitted to the EMBL Data Library, March 1996  
A:Reference number: T22439  
A:Accession: T22439  
A:Status: preliminary; translated from GB/EMBL/DDB  
A:Molecule type: DNA  
A:Residues: 1-213 <WII>  
A:Cross-references: EMBL:T20308; PIDN:CAA94351.1; GSPDB:GN00022; CESP:F49E11.4  
A:Experimental source: clone F49E11  
C:Genetics:  
A:Map position: 4  
A:Introns: 14/1; 60/3; 105/3; 175/2  
C:Superfamily: yellowjacket venom allergen 5

Query Match 15.3%; Score 153; DB 2; Length 213;  
Best Local Similarity 27.1%; Pred. No. 2.3e-06;  
Matches 45; Conservative 29; Mismatches 64; Indels 28; Gaps 7;

QY 24 LHNNGYRAFA-----RNKYSKMTWYDCTLEERAKYSAKSCSEEPS---SEEN 71  
DB 31 VHNFRSOLALGOLSPRGVKKPSASAMRKISMSKLLNATKFAETCRKNSVYMNATGES 90  
QY 72 VDVFSATLNIPL-----AGNSMSEIFEELRG---KYNNKNGKTSNIANN---VWDSHDK 121  
DB 91 IFMHRSSSLSPEDQVTLAPQKWNNE-FETNGMSLILYNNASROIGHAVOMAMHTTS 149  
QY 122 LCAVVDGSGKTH-----VWCOYGPPEAKGDKTYEEKAPCSRSDG 162

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Db      150 VCGGYSKCAVGPETQMTWVVCYFPGKNGIEEPYNGEFTCKPCE 195

RESULT 6
T22437
hypothetical protein F49E11.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T22437
R:Baynes, C
submitted to the EMBL Data Library, March 1996
A:Reference number: Z19564
A:Accession: T22437
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-212 <MIL>
A:Cross-references: EMBL:Z70308; PIDN:CA94349.1; GSPDB:GN00022; CESP:F49E11.5
C:Genetics:
A:Experimental source: clone F49E11
A:Gene: CESP:F49E11.5
A:Map position: 4
A:Introns: 17/1, 146/3, 180/2
C:Superfamily: yellowjacket venom allergen antigen 5

Query Match      15.2%; Score 152; DB 2; Length 212;
Best Local Similarity 24.5%; Pred. No. 2.8e-06;
Matches 51; Conservative 25; Mismatches 92; Indels 40; Gaps 8

OY      4 YSLCQQRKLTDDMRREFTELNNGRAFA-----RNYKTSKMTWYDDTLEEK 54
Db      13 FSPCTTCEFESEGNKYVILSRHNYLRSGIALGKRYVAGNSTRPSASNMKMLMDTLETTA 72
OY      55 YKSAKCSSEPSSEENV-----VPSATNLINPLEAGNSWSEIFELGKYVK 104
Db      73 QYSGTCPTGHSASRANIGENNYMTSPVYQTDAELLGRSANLMESE-FQRGC--WNG 129
OY      105 NKKTSNLTAN-----NMWDSHDLGAYVDCSGKTH-----YVCQYSPKAKDCKTY 151
Db      130 NLTFELPFGSIGAHQAMAMATNTKIGGICSGSDSFGQYVYVCLXSPAGNTGMDIT 189
OY      152 EERGAPGSCSPYAGVYTCDDDMQNLCT 179
Db      190 KSGETCSNCPD---GNCSS--STGLCV 212

RESULT 7
T19852
hypothetical protein C39E9.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T19852
R:Sims, M.
submitted to the EMBL Data Library, March 1996
A:Reference number: Z19187
A:Accession: T19852
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-208 <MIL>
A:Cross-references: EMBL:Z70307; PIDN:CA94335.1; GSPDB:GN00022; CESP:C39E9.2
C:Genetics:
A:Gene: CESP:C39E9.2
A:Map position: 4
A:Introns: 14/1, 59/3, 176/2
C:Superfamily: yellowjacket venom allergen antigen 5

Query Match      14.7%; Score 146.5; DB 2; Length 208;
Best Local Similarity 24.3%; Pred. No. 8.5e-06;
Matches 45; Conservative 26; Mismatches 63; Indels 51; Gaps 7

OY      24 LHNGRAAFANRYKTSK-----KFTWYDDTLEEKYKSAKCSSE----- 64
Db      30 VHNLTSLRNKIGTYVAGTAKPAASDMLKKMKMPATVAASNAQVANKRCPTGHSAGAGIGEN 89

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QY	65	-----PSSEENVVFSANALNPLP	AGNSWSEIFELRLGKYNNKNGKTSNAN	-----	113
Db	90	LYWWTISATITIDIOFGA-----	-TGSAAAMKEFPQDQ--WSSNLTLSMSLFNTGIGHA		139
QY	114	---MYMPSHDKLAGCAVNDCS-----	GFRHVVCQYGPFAKGGKTIYEAGAPCSRSDYGA		165
Db	140	TOAMAAKNTLIGCGVKNCKGDRNGFNKVTVVCQY	KFGQNYLNOMIYTSGTGSKCP---S		196
QY	166	GVTC	170		
Db	197	GTSC	201		

RESULT 8  
T22438  
hypothetical protein f49e11.6 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
C:Accession: T22438  
R:Bynes, C  
submitted to the EMBL Data Library, March 1996  
A:Reference number: Z19564  
A:Accession: T22438  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-207 <MID>  
A:Cross-References: EMBL:Z70308; PIDD:CAA94350.1; GSPDB:GN00022; CESP:f49e11.6  
A:Experimental source: clone f49e11  
A:Genetics:  
A:Gene: CESP:f49e11.6  
A:Map position: 4  
A:Introns: 58/3; 104/3; 176/2  
C:Superfamily: yellowjacket venom allergen antigen 5

Query Match	14.38;	Score 143;	DB 2;	Length 207;
Best Local Similarity	23.04;	Pred. No. 1.7e-05;		
Matches	46;	Conservative	24;	Mismatches 62; Indels 68; Gaps 8

QY	18	REMFELHNGRTAAFAFNNKYSK-----	NRIVYDCTLEKAKYSAEKSEPSSE	68
Db	23	QQAIVDAHNKLRSSIAKGYVAKGTQSGSNMRKIKMDAVATSAQNVANTC--	PTGH	79
QY	69	EE-----	NDVFSATILNIDLEAGNSWNSSEIFELRLGKYNNKNGKTSN	110
Db	80	SQSGSGYENLYWYMTSGTIGNLDFGPA-----	ASSMSWE-----	FOYGMTSN 124
QY	111	-----	TANWMDPSHDKLAGCAVNDCS-----	GFRHVVCQYGPFAKGGKTI 150
Db	125	TIDMTFNTGTGHAHQAMANFAALIGCGVKNCKGDRNSNGYKKNVAVVCQYRTGYNLNQPI		184
QY	151	YEGACPSRCSDYGAGVTC	170	
Db	185	YQGGTCAACP---SGNACD	201	

RESULT 9  
T19849  
hypothetical protein C39E9.6 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
C:Accession: T19849  
R:Stims, M  
submitted to the EMBL Data Library, March 1996  
A:Reference number: Z19187  
A:Accession: T19849  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-210 <MID>  
A:Cross-References: EMBL:Z70307; PIDD:CAA94332.1; GSPDB:GN00022; CESP:C39E9.6  
A:Experimental source: clone C39E9  
A:Genetics:  
A:Gene: CESP:C39E9.6

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A:Map position: 4
A:Introns: 58/3; 178/2
C:Superfamily: yellowJacket venom allergen 5

Query Match
Best Local Similarity 24.2%; Score 142; DB 2; Length 210;
Matches 48; Conservative 23; Mismatches 70; Indels 52; Gaps 8;

Oy 18 REMTEELHNQRYAAR-YY-----KSKRMVYVCCITLKKAKSKSEKSEPSSE 68
Db 22 KOSLIAMHNDIRIRIKGYIAKKNKRESATNWLAKKMSLSLSQNTYANGCHQHSTN 82
Oy 69 EBNV-----DYFS-----AATLNIPLKAGNSWSETEPLKCKATYN-----N 105
Db 83 DATTGEBNLYEMSGDEFSDLDFKFKITVA-----WDEFEQSGMNSNFSLALN 133
Oy 106 GKTSNIAMWYSDHDXLGCAYVDSG-----KTHVVCQYGPENAGDKRTIYEGAPC 157
Db 134 TGVAAATQIIMADPTGKIGGVAKNGCRDARRGGLFQYAIVCQYRVANGNEFFKNTYNSGATC 193
Oy 158 SKCSDYAGAVTCD 170
Db 194 SACP---AGTSC 203

RESULT 10
T19859
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T19859; T22441
R:Sims, M.
submitted to the EMBL Data Library, March 1996
A:Reference number: 219187
A:Accession: T19859
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-211 <W11>
A:Cross-references: EMBL:Z70307; PIDN:CA94341.1; GSPDB:GN00022; CESP:F49E11.111
R:Experimental source: clone C3959
R:Baynes C
submitted to the EMBL Data Library, March 1996
A:Reference number: 219564
A:Accession: T22441
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-211 <W12>
A:Cross-references: EMBL:Z70308; PIDN:CA94354.1; GSPDB:GN00022; CESP:F49E11.111
A:Experimental source: clone F49E11
C:Genetics:
A:Gene: CESP:F49E11.11
A:Map position: 4
A:Introns: 15/1; 60/3; 179/2
C:Superfamily: yellowJacket venom allergen antigen 5

Query Match
Best Local Similarity 24.0%; Score 140.5; DB 2; Length 211;
Matches 47; Conservative 25; Mismatches 71; Indels 53; Gaps 8;

Oy 15 DDMREMTLHNQRYAARFARNKTSKRT-----WVYVCCITEEKAYKSKSEKSEPP 65
Db 22 ESTGOFTVDLHNKLTSLAKGTYVAKGPTRAAGSNLTKKKMOTLTAAQTAFANTCPRGH 81
Oy 66 SSEE---EN-----VDVSAATINILLEGNSWSETEPLKRGVYKKNKSTN 110
Db 82 SNAAGVGENLYKRWSSLPSSGDIYG-----AASVAMQEPQOYG--WTTNFTQA 131
Oy 111 IAN-----WVWSDHDXLGCAYVDS-----GKTHVVCQYGPENAGDKRTIYEG 154
Db 132 LANRIGIATQMAATGILIGGVAKNGCRDPELNTNRYAVVCCQYKAGNSITLGDITKSG 191
Oy 155 ACRSCSDYAGAVTCD 170

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Db      192 TTCACAP---TGTTCE 204

RESULT 11
T24854
hypothetical protein T12A7.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #ext_change 15-Oct-1999
C:Accession: T24854
R:lemard, N
submitted to the EMBL Data Library, June 1996
A:Reference number: T19943
A:Accession: T24854
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-262 <N1>
A:Cross-references: EMBL:Z73911, PIDN:CA98140.1; GSPDB:GN00022; CESP:T12A7.3
A:Experimental source: clone T12A7
C:Genetics:
A:Gene: C3P:T12A7.3
A:Map position: 4
A:Introns: 86/2, 192/3, 231/2

Query Match      13.9%; Score 139; DB 2; Length 262;
Best Local Similarity 26.2%; Pred. No. 5.3e-05;
Matches 59; Conservative 20; Mismatches 66; Indels 80; Gaps 11.

OY      14 DDDREKETE---LHNGY-----RAAFARNYKT-----SKRRTMYDCTL 50.
Db      59 DEDDEHEFMENEVAFCNDGNCNNYVPPGSQLAG-NFYVTRRRTKRAAGSNIRKFFVNNATL 117
OY      51 EKAYKSAEKCESEPESEBEENVDFSAATLNIPLLEAGNSW-----S 92
Db      118 ERSAYSPFAOK--NPQSIS-----FIPDIGELFMHWSTRPDFENKYGPMAALS 163
OY      93 EIFELARKVYKNGKTSNI-----ANNVYDSHDKLCAVYDCS-----GKTH 134
Db      164 WIKFERKRFQDSNILNDLFGSGVGHATQVYADYQMKCAVSHKRIHKRTGRPTIKIC 223
OY      135 VVCYQGEAAGDGKITYEKGARFSCSDYDAGVTCDDQMNLLCI 179
Db      224 VCYHWPKRGNYLNEPIYLEGPGSKCE---SKKCDK-RIGLCI 262

RESULT 12
T19848
hypothetical protein C39E9.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #ext_change 18-Feb-2000
C:Accession: T19848
R:Sims, M.
submitted to the EMBL Data Library, March 1996
A:Reference number: T219187
A:Accession: T19848
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-209 <N1>
A:Cross-references: EMBL:Z70307; PIDN:CA94331.1; GSPDB:GN00022; CESP:C39E9.5
A:Experimental source: clone C39E9
C:Genetics:
A:Gene: C3P:C39E9.5
A:Map position: 4
A:Introns: 58/3, 177/2
C:Superfamily: yellowjacket venom allergen antigen 5

Query Match      13.9%; Score 138.5; DB 2; Length 209;
Best Local Similarity 24.7%; Pred. No. 4.5e-05;
Matches 46; Conservative 50; Mismatches 71; Indels 39; Gaps 7.

OY      18 REMFTELHNGYRAAFARNYKTSK-----NRIVYDCTLEEKAYKSAEKCESEPESE 68
Db      23 KQSVNNAHNVNRSISLAKGKGYVAKGTCKDASTNNLKKRWKUNSLDASQNVYNGCPMDHSPD 82

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OY 69 EBNVDVFSAAATNIPF-----EAGNSMSEIFELRGKYNKNGKTSNIAN----- 113  
 DB 83 KSYGNLTFMAYSSPPTDIDKLYOSAVDTWSE-FOHFG--NNSKFTTALMNTGIGHAT 139  
 OY 114 -MWDSDHDKLGCAVAVDC-----SGKTHVCOYGPPEAKGDKGKTIYEGAPCSDYGC 164  
 DB 140 OAVSAGVGCGCAKNCAGADSVRVGSKATVCOYKVPGNLYFNKYNYSAGKSCACP--- 196  
 OY 165 AGVTC D 170  
 DB 197 AGTSC E 202

## RESULT 13

T19847  
 hypothetical protein C399.4 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
 C:Accession: T19847  
 R:Stim: M  
 submitted to the EMBL Data Library, March 1996  
 A:Reference number: Z19187  
 A:Accession: T19847  
 A:Status: preliminary; translated from GB/EMBL/DBD  
 A:Molecule type: DNA  
 A:Residues: 1-209 <MTL>  
 A:Cross-references: EMBL:Z70307; PIDN:CAA94330.1; GSPDB:GN00022; CESP:C399.4  
 A:Experimental source: clone C399  
 C:Genetics: CESP:C399.4  
 A:Map position: 4  
 A:Intons: 14/1: 60/3: 177/2  
 C:Superfamily: yellowjacket venom allergen 5

Query Match 13.88; Score 137.5; DB 2; Length 209;  
 Best Local Similarity 24.38; Pred. No. 5.5e-05;  
 Matches 46; Conservative 21; Mismatches 75; Indels 47; Gaps 7;

OY 18 REMFTEHNGYRAAFARNTKT-----SKMTWYCTLEKAYSAKCS----- 62  
 DB 25 QOFTVDLHNSFRKLTGTYSINGTLKPAGSNIRKMSDSTLATSQYVANTCPTGFSWT 84  
 OY 63 -----EESPSEENVDFSAATLNIPLFAGNSMSEIFELRGKYNKNGK----- 107  
 DB 85 QGTGENLYWRTTSANISGLDIYGCA-----ASVSEOE-FOKYGATNYFSGELPFG 136  
 OY 108 TSNIANVWMDSHDKLGCAVAVDC-----GKTHVCOYGPPEAKGDKGKTIYEGAPCSDYGC 161  
 DB 137 VONGQMAWAKTLYVCGGVKNGCKDSGLNKVAVVCHYRPLGRYVDQMITVAGTSCGCP 196  
 OY 162 DYAGVTC D 170  
 DB 197 ---GTSC D 202

## RESULT 14

B33329  
 cysteine-rich secretory protein 2 type I precursor - human  
 N:Alternate names: testis-specific protein  
 C:Species: Homo sapiens (hmn)  
 C:Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 20-Jun-2000  
 C:Accession: B33329; S68682  
 R:Kasahara, N.; Galkin, J.; Brew, K.; Spurr, N.; Goodfellow, P.N.  
 Genomics 3, 527-534, 1989  
 A:Title: Cloning and mapping of a testis-specific gene with sequence similarity to a sp  
 A:Reference number: A33329; MUID:90129048; PMID:2613336  
 A:Accession: B33329  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-243 <KKS>  
 A:Cross-references: GB:M25532; NID:g339882; PIDN:AAA61220.1; PID:g339883  
 R:Kraetzschmar, J.; Haendler, B.; Eberspaecher, U.; Roosterman, D.; Donner, P.; Schleu  
 Eur. J. Biochem. 236, 827-836, 1996

A:Title: The human cysteine-rich secretory protein (CRISP) family. Primary structur  
 A:Reference number: S68682; MUID:96270732; PMID:8665901  
 A:Accession: S68682  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-243 <KRA>  
 A:Cross-references: EMBL:X95239; NID:g1262816; PIDN:CAA64526.1; PID:g1262817  
 C:Genetics: GDB:TPX1  
 A:Gene: GDB:TPX1  
 A:Cross-references: GDB:120760; OMIM:187430  
 A:Map position: 6p21-6qter  
 C:Superfamily: cysteine-rich secretory protein 1  
 F:1-20/Domains: signal sequence #status predicted <SIG>  
 F:21-243/Product: cysteine-rich secretory protein 2 type I #status predicted <MAT>

Query Match 13.78; Score 137; DB 2; Length 243;  
 Best Local Similarity 26.58; Pred. No. 7.3e-05;  
 Matches 49; Conservative 28; Mismatches 72; Indels 36; Gaps 9;

OY 18 REMFTEHNGYRAAFARNTKTSMRTWYCTLEKAYSAKCSSEEPSEEE----- 70  
 DB 38 REIYNK-HNELKKAISP--PASNMLKEMNSREVTTNAQRMANKCTIQHSDPEDRTSTRC 94  
 OY 71 NVDVFSAAATLNIPLFAGNSMSEIFELRGKYNKNGKTSN-----IANVWMDSHDKLCA 125  
 DB 95 GENLYSSDPISWSSALOSWYDELDF---VYGVGPKSPNAVGHYTLQWYSTYVQVCG 151  
 OY 126 VDC-----SGKTHVCOYGPPEAKGDK--TIYEGAPCSDYAGVTC D-----D 172  
 DB 152 IAYCPNQDLSLKYVCOYCPAGNNNRKNTPYOQCTPCACPD-----DCDGLCTNSCQ 206  
 OY 173 WQNL 177  
 DB 207 YODL 211

## RESULT 15

T22432  
 hypothetical protein F49E11.10 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
 C:Accession: T22432  
 R:Baynes, C.  
 submitted to the EMBL Data Library, March 1996  
 A:Reference number: Z19564  
 A:Accession: T22432  
 A:Status: preliminary; translated from GB/EMBL/DBD  
 A:Molecule type: DNA  
 A:Residues: 1-207 <MTL>  
 A:Cross-references: EMBL:Z70308; PIDN:CAA94344.1; GSPDB:GN00022; CESP:F49E11.10  
 A:Experimental source: clone F49E11  
 C:Genetics: CESP:F49E11.10  
 A:Map position: 4  
 A:Intons: 58/3: 104/3: 175/2  
 C:Superfamily: yellowjacket venom allergen 5

Query Match 13.48; Score 133.5; DB 2; Length 207;  
 Best Local Similarity 26.18; Pred. No. 0.00012;  
 Matches 46; Conservative 23; Mismatches 72; Indels 35; Gaps 7;

OY 25 HNGYRAAFARNTKT-----MRTWYCTLEKAYSAKCSSEEPSEEE---BNV 72  
 DB 30 HNTLRKIRKIGTYAKGTQKSPETNLLKKMDSAVVAAVNAWNGCPTGSHSDAGLGNL 89  
 OY 73 DVF-----SAATLNIPLFAGNSMSEIFELRGKYNKNGKTSNIAN-----MWDSDH 120  
 DB 90 YWYVTSIGSLGDLNLYGSAASWKEFDYD--WKSNIATIDIFNTGIGHATONAMKSN 147  
 OY 121 KLCAVAVDC-----GKTHVCOYGPPEAKGDKGKTIYEGAPCSDYAGVTC D 170  
 DB 148 LIICGVKDCGDSNGLNKVAVVCHYRPLGRYVDQMITVAGTSCGCP---SSTSC E 200

RESULT 16  
neutrophil granules matrix glycoprotein SGP28 precursor - human  
C/Species: Homo sapiens (man)  
C/Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 17-Nov-2000  
C/Accession: S68691; S74313; S68683  
R/Jeldsen, L.; Cowland, J.B.; Johnsen, A.H.; Borregaard, N.  
FEBS Lett. 380: 246-250, 1996  
A/Title: SGP28, a novel matrix glycoprotein in specific granules of human neutrophils  
A/Reference number: S68691; MUID:96186934; PMID:8601434  
A/Accession: S68691  
A/Molecule type: mRNA  
A/Residues: 1-245 <KJE>  
A/Cross-references: EMBL:X94323; NID:g1213612; PID:CAA63984.1; PID:g1213613  
A/Accession: S74313  
A/Molecule type: protein  
A/Residues: 33-83;96-143;165-217;221-226 <KJL>  
R/Kretzschmar, J.; Haendler, B.; Eberspacher, U.; Roosterman, D.; Donner, P.; Schleut  
Eur. J. Biochem. 236: 827-836, 1996  
A/Title: The human cysteine-rich secretory protein (CRISP) family. Primary structure and  
A/Reference number: S68681; MUID:96270732; PMID:8665901  
A/Accession: S68683  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-105; 'S', 107-245 <KRA>  
A/Cross-references: EMBL:X95240; NID:g1262818; PID:CAA64527.1; PID:g1262819  
C/Genetics: SGP28  
A/Suprafamily: cysteine-rich secretory protein 1  
F/19/Domains: signal sequence #status predicted <ANT>  
F/20-245/Product: neutrophil granules matrix glycoprotein SGP28 #status predicted <ANT>  
Query Match 13.2%; Score 132; DB 2; Length 245;  
Best Local Similarity 25.1%; Pred. No. 0.00021;  
Matches 48; Conservative 22; Mismatches 77; Indels 44; Gaps 8;  
14 DDDKREMEFT-----HNGYRAA--ARKYTSKRMVYDCTLEKAYK 56  
DB 21 NEDNDPFTLLTTOQVOREIVAKKHELRRAVSPARR-----MLKKNKKDAANAKK 75  
QY 57 SAECSESESEENVDFSAATNIPLEAGNSMSEIFELRGVYN-----KNG 106  
DB 76 WANCNTRHSNFRDRTSLKCGE-NLYMSAPSSMSQALQSWFDYDFDGVGPKTPNA 134  
QY 107 KTSNIAMVWDSDHKLGAAYVDCSG---KTHVCCYGPGEAKGDKTI--YEGAPCSRC 160  
DB 135 VGHYQVWYSSYLGVCGMAVCPNOKVLEKTYVYCYCPAGNMANRUYVPEEGAPCASC 194  
QY 161 SDYGAAYTCD 171  
DB 195 PD-----NCDD 200

RESULT 17  
A33329  
testis-specific protein - mouse  
C/Species: Mus musculus (house mouse)  
C/Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 29-Sep-1999  
C/Accession: A33329  
R/Raschke, M.; Gultknecht, J.; Brew, K.; Spurr, N.; Goodfellow, P.N.  
Genomics 5: 527-534, 1989  
A/Title: Cloning and mapping of a testis-specific gene with sequence similarity to a spe  
A/Reference number: A33329; MUID:90129048; PMID:2613236  
A/Accession: A33329  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-243 <RAS>  
A/Cross-references: GB:M25533; NID:g202126; PID:AAA0472.1; PID:g202127  
C/Suprafamily: cysteine-rich secretory protein 1  
Query Match 12.7%; Score 127; DB 2; Length 243;  
Best Local Similarity 24.9%; Pred. No. 0.00058;

Matches 49; Conservative 28; Mismatches 84; Indels 36; Gaps 9;  
QY 11 EKIDDDREMEFT-----ELNGYRAAPARNYKTSKRMVYDCTLEKAYKSAEK 60  
DB 21 EGDNDPFTSLTNOLOQVOREIVAKKHELRRAVSPARR-----MLKKNKKDAANAKK 78  
QY 61 CSEPSSESEENVDFSAATNIPLEAGNSMSEIFELRGVYN-----KTSNIA- 112  
DB 79 CLEHSSKDDR-KINIRCGENLWSTDTPLMSTVIO---SWYENEDFYGVGAKPNSAV 134  
QY 113 ---NMVWSDHKLGAAYVDCSGKTHV---VCOYGPGEAKGDK--TIYEGAPCSRCSD 162  
DB 135 GHYQVWYSSYLVGCGMAVCPNOKVLEKTYVYCYCPAGNMANRUYVPEEGAPCASC 194  
QY 163 YGAGVYTCDD--DMQNL 177  
DB 195 NCBNGCTNSCDFEDL 211

RESULT 18  
T27833  
hypothetical protein ZK384.1 - Caenorhabditis elegans  
C/Species: Caenorhabditis elegans  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
C/Accession: T27833  
R/Almscouph, R.  
submitted to the EMBL Data Library, November 1996  
A/Reference number: Z20427  
A/Accession: T27833  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-156 <KTI>  
A/Cross-references: EMBL:Z82092; PID:CA805010.1; GSPDB:GN00023; CESP:ZK384.1  
A/Experimental source: clone ZK384  
C/Genetics: ZK384  
A/Map position: 59/3; 95/3; 157/2  
A/Intros: 58/3; 95/3; 157/2  
C/Suprafamily: yellowjacket venom allergen antigen 5  
Query Match 12.4%; Score 124; DB 2; Length 196;  
Best Local Similarity 24.8%; Pred. No. 0.00082;  
Matches 41; Conservative 25; Mismatches 77; Indels 22; Gaps 7;  
12 KIDDDREMEFTELNGYRAAPARNYKTS-----KMTVYDCTLEKAYKSAEKS 62  
DB 17 QLSPNRQOVLDFHNKLRSQLGVFSANGTIRKPPARMERLYGOOFERLADYVADCP 76  
QY 63 ---EPPSSESEENVDFSAATNIPLEAGNSMSEIFELRG---KYNNKNGKTSNIAMVW 116  
DB 77 DGLEIPIGRNIGMNYTTRKV---IDALND-WAEFPVNCMLSTIYN-DTSSISAASQMV 130  
QY 117 DSHDKLGAAYVDCSG-KTHVCCYGPGEAKGDKTIYEGAPCSRC 160  
DB 131 AGTKYVCGVRCDPINVVVYCYQGNLVGRPIYREKGPCTAC 175

RESULT 19  
JC5308  
testis-specific, vespid, and pathogenesis-related protein 1 precursor - human  
C/Species: Homo sapiens (man)  
C/Date: 01-May-1997 #sequence\_revision 01-May-1997 #text\_change 19-May-2000  
C/Accession: JC5308; PC4311  
R/Rich, T.; Chen, P.; Furman, F.; Huynh, N.; Israel, M.A.  
Gene 180: 125-130, 1996  
A/Title: RVP-1, a novel human gene with sequence similarity to genes of diverse spe  
A/Reference number: JC5308; MUID:97128816; PMID:8973356  
A/Accession: JC5308  
A/Molecule type: mRNA  
A/Residues: 1-266 <RCIC>  
A/Cross-references: EMBL:X91911; NID:g1030052; PID:CAA63005.1; PID:g1030053  
A/Accession: PC4311  
A/Molecule type: protein



Db 78 KLHPNTSGENITWGSPIFVS-----AIIWVDEIODIFKRLCKKVCCHYOV 131  
 QY 115 VMSHRLCCAVDC-----SGKTHVCOGPEPKGDKT-IYEGAPCSRCSDY 164  
 Db 132 VMDSTKVCACVQPEPKVSGDLSNGAFICNYGP--GNYPTWPKRGACSCAPN-- 187  
 QY 165 AGVTCDDDMQNLCT 179  
 Db 188 -----NDKCLDNLCV 197

RESULT 23  
 JE0204  
 testicular protein Tpx-1 - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 21-Aug-1998 #sequence\_revision 21-Aug-1998 #text\_change 21-Jul-2000  
 C:Accession: JE0204  
 R:Maeda, T.; Sakashita, M.; Ohba, Y.; Nakaniishi, Y.  
 Biochem. Biophys. Res. Commun. 248, 140-146, 1998  
 A:Title: Molecular cloning of the rat tpx-1 responsible for the interaction between sperm and egg  
 A:Reference number: JE0204; PMID:98340864; PMID:9675100  
 A:Accession: JE0204  
 A:Molecule type: mRNA  
 A:Residues: 1-243 <AAE>  
 A:Cross-references: DDBJ:AB009662; NID:93374579; PIDN:BA32029.1; PID:93374580  
 C:Comment: This protein functions as a cell adhesion protein for the association between sperm and egg  
 C:Genetics:  
 A:Map position: 17  
 A:Superfamily: cysteine-rich secretory protein 1

Query Match 12.1%; Score 121; DB 2; Length 243;  
 Best Local Similarity 25.2%; Pred. No. 0.0027; Mismatches 66; Indels 32; Gaps 8;  
 Matches 41; Conservative 24; Mismatches 66; Indels 32; Gaps 8;

QY 39 SKRRTVYCTLEKAYKSAEC-SEPSSEENDVSAATLNIPLKACN-----SNW 91  
 Db 57 SNLKEHNVQAAAKAKNANCLHSESTEDKINICGSLNLSIDPISMTYIQSMY 116  
 QY 92 SE-----IFLRKRYTNKGTSNINAWYDSDHDKGCAVDCSG---KTHVCOGPEA 143  
 Db 117 EENENFVGVGAK--PSAVGHITQLVWTSFSGKVCVATCPNODTLKIFYVCHICPMG 173  
 QY 144 KGDKG--TIYEGAPCSRCSDYAGVTCDD-----DMQNL 177  
 Db 174 NNVKSTPYHGTGTCACSPN-----NCNGLCTNSCDFDL 211

RESULT 24  
 A49202  
 cysteine-rich secretory protein-1 - mouse  
 N:Alternate names: CRISP-1  
 C:Species: Mus musculus (house mouse)  
 C:Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 29-Sep-1999  
 C:Accession: A49202  
 R:Haendler, B.; Kratzschmar, J.; Theuring, F.; Schlemming, W.D.  
 Endocrinology 133, 192-198, 1993  
 A:Title: Transcripts for cysteine-rich secretory protein-1 (CRISP-1; DE/AEG) and the novel secretory protein-2 (SP-2) in the developing mouse ovary  
 A:Reference number: A49202; PMID:93307144; PMID:9319566  
 A:Accession: A49202  
 A:Status: preliminary  
 A:Molecule type: nucleic acid  
 A:Residues: 1-244 <AAE>  
 A:Cross-references: GB:105559; NID:9309190; PIDN:AAA3760.1; PID:9309191  
 A:Experimental source: NMR, epididymal, salivary gland  
 A:Title: Sequence extracted from NCI backbone (NCBIN:134675, NCBI:134676)  
 C:Superfamily: cysteine-rich secretory protein 1

Query Match 12.0%; Score 119.5; DB 2; Length 244;  
 Best Local Similarity 25.4%; Pred. No. 0.0027; Mismatches 64; Indels 35; Gaps 10;  
 Matches 51; Conservative 31; Mismatches 64; Indels 35; Gaps 10;

QY 3 DYSLCOORREKDD---DMRETFELHNGRAFAFANYTSMKRMVYDCTLEKAYKSAE 59

Db 21 DSGENRLEKSTFKNSVOELIVSKHNOLRNWSPPS--GSDLLKKNRYDAQVNAQMD 78  
 QY 60 KCEPSESE-----ENDVFAATLNIPLKAGNSMSEIFELRGVYKN--NGK 108  
 Db 79 KTFESHPIELRTNLRGEN--LFKSSYLASMSAIOGMVYEDLYDVGPRQPSVY 136  
 QY 109 SNIANWVDSHDKLCAVDCSG---KTHVCOGPEPKGDKT-IYEGAPCSRCSDY 163  
 Db 137 GHYTOVWNSFPVACGVAECPRNPLRYRYCHCPGVYQGRLYPTPTAGEPCASCPDH 196  
 QY 164 GAGVTCDDDMQNLCT--IGH 181  
 Db 197 -----CEDG-----LCTNSCGH 208

RESULT 25  
 T52399  
 pathogenesis-related protein homolog [imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 24-Oct-2000 #sequence\_revision 24-Oct-2000 #text\_change 03-Nov-2000  
 C:Accession: T52399  
 R:Kaneko, T.; Kato, T.; Sato, S.; Nakamura, Y.; Asanikazu, E.; Tabata, S.  
 submitted to the EMBL Data Library, September 1999  
 A:Reference number: 226062  
 A:Accession: T52399  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-161 <KAD>  
 A:Cross-references: EMBL:AF000417; PIDN:BA802556.1  
 A:Experimental source: cultivar Columbia  
 C:Genetics:  
 A:Map position: 3  
 A:Superfamily: pathogenesis-related leaf protein

Query Match 11.8%; Score 118; DB 2; Length 161;  
 Best Local Similarity 26.1%; Pred. No. 0.0022; Mismatches 41; Indels 54; Gaps 8;  
 Matches 41; Conservative 21; Mismatches 41; Indels 54; Gaps 8;

QY 13 LDDDEREFTELHNGR-----AFARNYTSKRTVYDCTL----- 50  
 Db 21 LAEDLDQDFLEAHNEARNENGVLDPLWMDVYAAVIAVSNOR---INDCALVHNSGPEG 76  
 QY 51 EERAYKSAKCESEPS---SEENVDFSAATLNIPLKAGNSMSEIFELRGVYKN 106  
 Db 77 ENIAWSSGMSADDAEMWINEKQYTD-YDSNTCNDP-----NG 114

QY 107 KTS-NIANWVDSHDKLCAVDC--SGKTHVCOGPEA 141  
 Db 115 GTCLEHYVWKNVRLGCAKAVVCSGCTFTICNDP 151

RESULT 26  
 D86143  
 hypothetical protein F6p3.11 - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Dec-2001  
 C:Accession: D86143  
 R:Thoenig, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Aloni, C.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, A.; Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzli, R.; Mitter, M.; Rooney, T.; Rowley, D.; Sakano, H.; Schmitz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tait, J.; Tait, J.; Yu, D.; Yu, G.; Fraser, C.M.; Venturi, J.C.; Davis, R.W.  
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis thaliana  
 A:Reference number: A86141; PMID:21016719; PMID:11130712  
 A:Accession: D86143  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-263 <STO>  
 A:Cross-references: GB:AE005172; NID:99665145; PIDN:AAF97329.1; GSPDB:GN00141

C:Genetics:  
A:Map position: 1

Query Match 11.8%; Score 118; DB 2; Length 283;  
Best Local Similarity 25.8%; Pred. No. 0.0044;  
Matches 41; Conservative 22; Mismatches 60; Indels 36; Gaps 8;

QY 8 OOREKLDMDMEMTELHN-----GYRAAFRRNYKTSKMTWYDCTLEEK 53  
DB 118 RRRNVNRAARE-FLIHNIVRARVGEPPQMDRLAAVFTWANGR---VGCRLVH- 171  
QY 54 AKSAEKSEEPSESEENVDFSAATLN-ILEAGNSWSE--IPELGRKYNNKNGTSN 110  
DB 172 -----SNCPYGE-----NIFMAGKNMSPRDIVNMDDEKFDVGNCEPHHCGH 219  
QY 111 IANWYDSDHDLGCAVYDCS-GKTHVCOYGPBEAKGDKGK 148  
DB 220 YTOIVNRDSTKVGCAVDCSNGVYALCVNPPONTGE 258

## RESULT 27

T04989

pathogenesis-related protein 1 precursor, 19.3k - Arabidopsis thaliana  
N:Alternate names: protein T16L1.210

C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 23-Apr-1998 #sequence\_revision 23-Apr-1999 #text\_change 20-Jun-2000  
C:Accession: T04989; S71271  
R:Bayan, R.; Obermaier, B.; Deutschenbaur, S.; Piravandi, E.; Hohnleisel, J.; Mewes, H.W.;  
submitted to the Protein Sequence Database, November 1998  
A:Reference number: 215393  
A:Accession: T04989  
A:Molecule type: DNA  
A:Residues: 1-163 <BEV>  
A:Cross-references: EMBL:AL031394  
A:Experimental source: cultivar Columbia; BAC clone T16L1  
R:Kloska, S.; Schuster, W.  
submitted to the EMBL Data Library, March 1996  
A:Reference number: S71271  
A:Accession: S71271  
A:Molecule type: DNA  
A:Residues: 1-77, 'P', '79-82', 'L', '84-88', 'RL', '91-92', 'RR', '95-162', 'LKENSIR' <KLO>  
A:Cross-references: EMBL:X96600; NID:g1228948; PID:g1228950  
C:Genetics:  
A:Gene: PRI  
A:Map position: 4  
A:Note: T16L1.210  
C:Superfamily: pathogenesis-related leaf protein  
F:1.26/Domain: signal sequence #status predicted <SIG>  
F:27.163/Product: pathogenesis-related protein 1, 19.3k #status predicted <MAT>

Query Match 11.3%; Score 113; DB 2; Length 163;  
Best Local Similarity 24.1%; Pred. No. 0.0064;  
Matches 38; Conservative 23; Mismatches 53; Indels 44; Gaps 7;

QY 16 DMREMFTELHNGYR-----AAFAFYKTSKMTWYDCTLEEKAYKSEKC 61  
DB 28 DSPDFLAIVNRARAVYGVPLMDKDEYKAAANRANQKRG---DCAMKHS----- 76  
QY 62 SEEPSSEENVDFSAATLNIPLEAGNSWSEIFELGRKYNNKNGT-----SNIANM 114  
DB 77 -----GSTGENIANSSTMTGV--AAVDMWDEQFD-----YDSDNTCAMDKCGHATQV 125  
QY 115 VMDSHDRLGCAVYDCS-SGKTHVCOYGPBEAKGDKGKTY 151  
DB 126 VMNRSERLGCAVYDCSNGVYALCVNPPONTGE 163

## RESULT 28

A31085

antigen 5-2 precursor - bald-faced hornet  
C:Species: Vespaula maculata (bald-faced hornet)  
C:Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 11-Jan-2000  
C:Accession: A31085

R:Fang, K.S.Y.; Vitale, M.; Fehner, P.; King, T.P.  
Proc. Natl. Acad. Sci. U.S.A. 85, 895-899, 1988

A:Title: cDNA cloning and primary structure of a white-face hornet venom allergen,  
A:Reference number: A94213; MUID:88124947; PMID:3422469

A:Accession: A31085  
A:Molecule type: mRNA  
A:Residues: 1-227 <FRAN>  
A:Cross-references: GB:J03601; NID:g156714; PID:g156715  
C:Superfamily: yellowjacket venom allergen antigen 5  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-227/Product: antigen 5-2 #status predicted <MAT>

Query Match 11.3%; Score 112.5; DB 2; Length 227;  
Best Local Similarity 23.4%; Pred. No. 0.011; 74; Indels 27; Gaps 6;  
Matches 39; Conservative 27; Mismatches 50

QY 13 LDDMEFTELHNGYRAAFRRNYKTSKMTWYDCTLEEKAYKSEKC- 61  
DB 59 LTNDEKNEILKRNHDFKONVAKGLETRKRPQPPAKNNVNVNDELAKIQTWANOCD 118  
QY 62 -----SEEPSSEENVDFSAATLNIPLEAGNSWSEIFELGRKYNNKNGT-----KTS 109  
DB 119 FNHDDCRNPAKYQVGNIAISITTAQDFRPSKLIKQWEDVTEFNKYKQLQNSFRVVG 178  
QY 110 IANWYDSDHDLGCAVYDCS-GKTHVCOYGPBEAKGDKGKTY 152  
DB 179 HYQWYMGKTKKIKGSGIKYIEDNMYTHVLCVNGPGGNDPFIYE 225

## RESULT 29

T21763

hypothetical protein F35E12.1 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T21763  
R:Steward, C.  
submitted to the EMBL Data Library, November 1996  
A:Reference number: 219470  
A:Accession: T21763  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-385 <RIID>  
A:Experimental source: EMBL:281527; PID:CA04269.1; GSPDB:GN00023; CESP:F35E12.1  
C:Genetics:  
A:Gene: CESP.F35E12.1  
A:Map position: 5  
A:Intons: 103/71; 165/3; 210/3; 263/2; 342/2

Query Match 11.3%; Score 112.5; DB 2; Length 385;  
Best Local Similarity 24.7%; Pred. No. 0.02;  
Matches 36; Conservative 21; Mismatches 50; Indels 45; Gaps 7;

QY 23 ELHNGYRAAFRRNY-----KTSKMTWYDCTLEEKAYSAKSESE----- 64  
DB 135 KIHNDLRSEIAGLEFLAKIEKPPASDMKISMDSIASEQFTIEKCPMNHKTREYGEN 194  
QY 65 -----PSSEENVDFSAATLNIPLEAGNSWSEIFELGRKYNNKNGTSNAN--- 113  
DB 195 MHRWSKSEITDLDIYGT-----KRAESNAGE-FQKKGESNIYTKPTEKSGIGHATQ 246  
QY 114 VMDSHDRLGCAVYDCS-----GKTHVCOY 139  
DB 247 MWWSQAYLIGCGVCKGCPDRKTKRMKRIYVCRY 280

## RESULT 30

B44583

venom allergen antigen Ves g 5 - German yellowjacket  
C:Species: Vespaula germanica (German yellowjacket)  
C:Date: 27-Jun-1994 #sequence\_revision 27-Jun-1994 #text\_change 11-Jan-2000  
C:Accession: B44583; A44522  
R:Hoffman, D.R.





QY 18 REMTEIANGYRAAFRRNTK-----SKRTMYTDCLEKAYKSAKNC----- 61  
 DB 42 KOELIKTHNDPFRNKVARGLETNGNGPOPPAKNNMNLVNNMLANIAQIMASOCKGHDPT 101  
 QY 62 --SEPSSEENDVFSATNTIPLEAGN---SMWSEIFELRGKY---YNNKNGTSNIAN 113  
 DB 102 CKDTFTYNGONIAV--SSSTAAYVENGNLVKAMENEVDNPTLSMEONEFKIGHYTO 160  
 QY 114 WYWDSDHKLCA---VVDSCGKTH-VVCQYGPAAKGDGRTIVE 152  
 DB 161 WMAKTRKICGSGIKYVDNNMYTHLYCNGPAGNNGOEVYE 203

## RESULT 35

T27834  
 hypothetical protein ZK384.2 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
 C:Accession: T27834  
 R:Almscough, R.  
 submitted to the EMBL Data Library, November 1996  
 A:Reference number: 220427  
 A:Accession: T27834  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-212 <full>  
 A:Cross-references: EMBL:282092; PIDN:CAB05011.1; GSPDB:GN00023; CESP:ZK384.2  
 A:Experimental source: clone ZK384  
 C:Genetics:  
 A:Gene: CESP:ZK384.2  
 A:Map position: 5  
 A:Intons: 60/3; 106/3; 180/2  
 C:Superfamily: yellowjacket venom allergen antigen 5

Query Match 10.98; Score 108.5; DB 2; Length 212;  
 Best Local Similarity 23.98; Pred. No. 0.022; 75; Indels 51; Gaps 9;  
 Matches 47; Conservative 24; Mismatches 75

QY 9 OREIIDDMEFTELHNGYRAAFRRNTK-----KTSKRTMYTDCLEKAYKSAE 59  
 DB 25 QREIYD-----FHSLSQNLNGDIYDGYPPRAKDKAKKMPILLAGAKKNNAA 75  
 QY 60 KCSEPSSEENDVFSATNTIPLEAGN---SMWSEIFELRGKY---YNNKNGTSNIAN 102  
 DB 76 TC--PSLFTDSKMLGRNTYHRLANVYSGSLDKYALFAVKKWERO--FEERGMKNQEFRMF 131  
 QY 103 NKNGTSNIANWYWDSDHKLCAVYDCS-----GTHVVCQYGPAAKGDGRTIVE 153  
 DB 132 GDHRLTSAYQWYMATRHHVGGGVNICDAEKNLFGYRNRVVYICBYOSKGNHGLPYKE 191  
 QY 154 GAPCSRCSIDYAGAVTCD 170  
 DB 192 GPTCSACP---ASTKCE 205

## RESULT 36

B37329  
 antigen 5 - eastern yellowjacket  
 C:Species: Vespula maculifrons (eastern yellowjacket)  
 C>Date: 06-Nov-1992 #sequence\_revision 06-Nov-1992 #text\_change 11-Jan-2000  
 C:Accession: B37329  
 R:Li, G.; Villalba, M.; Coats, M.R.; Hoffman, D.R.; King, T.P.  
 submitted to the Protein Sequence Database, August 1992  
 A:Reference number: A37329  
 A:Accession: B37329  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-204 <full>  
 C:Superfamily: yellowjacket venom allergen antigen 5

Query Match 10.78; Score 107; DB 2; Length 204;  
 Best Local Similarity 21.68; Pred. No. 0.029; 70; Indels 34; Gaps 7;  
 Matches 58; Conservative 34; Mismatches 70

QY 4 YSLCQOREKIDDDREKFEFTELHNGYRAAFRRNTK-----SKRTMYTDCLEK 53  
 DB 34 YGLTKOERQ-DILKE-----HDFRQKTLARGLTRNGPPOPPAKNNMNLVNSDELAYI 86  
 QY 54 AYKSAEK-----SEPSSEENDVFSATNTIPLEAGNSMWSEIFELRGKY 102  
 DB 87 AQYMANOCQYGHDCRVDYARYQVGNVALTGSTAAYVNDPVKLVKMEDEVDYDPKRRF 146  
 QY 103 NKNG--KTSNIANWYWDSDHKLCA---VVDSCGKTHVVCQYGPAAKGDGRTIVE 152  
 DB 147 SENNFLKIGHTYQWYMATRHHVGGGVNICDAEKNLFGYRNRVVYICBYOSKGNHGLPYKE 202

## RESULT 37

T24999  
 hypothetical protein T19C9.5 - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 04-Mar-2000  
 C:Accession: T24999  
 R:Matthews, L.  
 submitted to the EMBL Data Library, March 1997  
 A:Reference number: 219967  
 A:Accession: T24999  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-212 <full>  
 A:Cross-references: EMBL:292972; PIDN:CAB07484.1; GSPDB:GN00023; CESP:T19C9.5  
 A:Experimental source: clone T19C9  
 C:Genetics:  
 A:Gene: CESP:T19C9.5  
 A:Map position: 5  
 A:Intons: 64/3; 109/3; 176/2  
 C:Superfamily: yellowjacket venom allergen antigen 5

Query Match 10.78; Score 107; DB 2; Length 212;  
 Best Local Similarity 18.78; Pred. No. 0.03; 58; Indels 58; Gaps 7;  
 Matches 35; Conservative 36; Mismatches 58

QY 24 LNHGYRAAFRRNTK-----KTSKRTMYTDCLEKAYKSAEKSEPSSEENDVFS 76  
 DB 37 IHNKLNKASHGELMRHSISKSMDLSMNSLVAENKRYC--EPADNK----- 87  
 QY 77 AATLNTIPLEAGNSMWSEIFELRGKYNNKNGTSNIANWYWDSDHKL----- 122  
 DB 88 ---NLPIKIDN---IYQDVNTYDDIDYGVGANGSINKDTHDLKSEAKAKNNRLROM 139  
 QY 123 -----GCAYVDCSGKTH---VVCQYGPAAKGDGRTIVEBGAPCSRSYGA 165  
 DB 140 LYSKSKSICCIYESCDKIDSKGINYMTLLICKYSPLENIDEKLDKGPSCNCP---S 196  
 QY 166 GYVCDDD 172  
 DB 197 GTSCGTD 203

## RESULT 38

A44583  
 venom allergen antigen Vea f 5 - yellowjacket (Vespula flavopilosa)  
 C:Species: Vespula flavopilosa  
 C>Date: 27-Jun-1994 #sequence\_revision 27-Jun-1994 #text\_change 11-Jan-2000  
 C:Accession: A44583; B44552  
 R:Hoffman, D.R.  
 J. Allergy Clin. Immunol. 92, 707-716, 1993  
 A:Title: Allergens in hymenoptera venom xxy: the amino acid sequences of antigen 5  
 A:Reference number: A44583; MUID:94044316; PMID:8227862  
 A:Accession: A44583  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-204 <full>  
 C:Superfamily: yellowjacket venom allergen antigen 5

Query Match 10.68; Score 106; DB 2; Length 204;





Tue Jul 15 09:48:48 2003

us-09-937-555a-2.rpr

Page 14

Search completed: July 15, 2003, 08:34:55  
Job time : 42 secs

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QY 57 SAECSEEPSESE---NDVFSATLNI-----PLEAGNSMSEIFE-----LNG 99
DB 287 HGNKCYAQSHGDEPRGJENIYRTSYLAKDKKAKAQSOLMNNKEKGVPSNVLT 346
QY 100 KYVKNKG-KTSMIANMWDSDHKLGCANVDCSGKTHVCOYGPAPKADGKTYIEGAPCS 158
DB 347 ALMNRFGMOIGHYTMADTYTKLGCAVVCNDFTFGVCOYGPAGNMGHVITMCPGCS 406
QY 159 RGSDDYAGVYC 169
DB 407 QCS---PGATC 414

RESULT 2
CRS3_HORSE
ID CRS3_HORSE STANDARD: PRT: 245 AA.
AC 019010:
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cysteine-rich secretory protein-3 precursor (CRISP-3).
GN CRISP3.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Ferissodactyla; Equidae; Equus.
OX NCBI_TaxID-9796;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Ampulla;
RX MEDLINE-98422318; PubMed-9748582;
RA Schumbody A., Gentzel M., Wolles H., Ralda M., Neumann U.,
RA Toefter-Petersen E.;
RT "Equine CRISP-3: primary structure and expression in the male genital
RL tract.";
RL Blochim. Biophys. Acta 1387:206-216(1998).
CC -1- SUBCELLULAR LOCATION: SECRETED; IN NEUTROPHILS. LOCALIZED IN
CC SPECIFIC GRANULES (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN THE SALIVARY GLAND. IN THE
CC AMPULLA AND THE SEMINAL VESICLE.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
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DB EMBL; AJ001400; CA004729.1; -
DR HSSP; P04284; ICFE.
DR InterPro; IP0001283; Allrgn_V5/TPX1.
DR Pfam; PF00188; SCP.1.
DR PRINTS; PR00837; V5TPXLIKE.
DR PRODOM; PD000542; Allrgn_V5/TPX1.1.
DR SMART; SM00198; SCP.1.
DR PROSITE; PS01009; SCP_AGS_PRL_SCP_1.1.
DR PROSITE; PS01010; SCP_AGS_PRL_SCP_2.1.
KW SIGNAL; Multigene family.
FT SIGNAL 1 22
FT CHAIN 23 245
SO SEQUENCE 245 AA; 27308 MW; 893AAE8F402BA22 CRC64;

Query Match 14.4%; Score 143.5; DB 1; Length 245;
Best Local Similarity 26.4%; Pred. No. 8e-06; 76; Indels 33; Gaps 8;
Matches 48; Conservative 25; Mismatch 33; Indels 33; Gaps 8;
QY 16 DAREFTELANCYRAAFARNTKTSKRTVYDCTLEKAYVSAKCSSEPSSEENV--- 72
DB 36 EVCKEYVNHNDLRTVSP--LASNMLKQWQSKTRATNAQWMAKCLLOHSAKEDRAVGT 93
QY 73 ----DVFSATLNIPLAGNSMSEIFEIRGKYVKNKGTSN-----IANVWDSDHKL 122

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DB 94 MKCGENLMSSTIPMSDIAIQWHDVDFK---YGVGRTPNAVGHYTYVWYSSYRV 150
QY 123 GCANVDC---SGKTHVCOYGPAPKADGK--TYIEGAPCSRCSDDYAGVTCDDQMQL 176
DB 151 GCGIAYCPKQGTLLKYYVCOYCPAGNMYNKNINFEQGTFCARCPG-----NCD---NG 201
QY 177 LC 178
DB 202 LC 203

RESULT 3
HELIO_HELIO
ID HELIO_HELIO STANDARD: PRT: 242 AA.
AC 091055;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Heliothermine precursor (HLTY).
DE Heloderma horridum horridum (Mexican beaded lizard).
OS Heloderma; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosaurs; Squamata; Scleroglossa; Anguilliformes; Helodermatidae;
OC Heloderma.
OX NCBI_TaxID-8552;
RN [1]
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RC TISSUE-Salivary gland;
RX MEDLINE-95375162; PubMed-7647234;
RA Morrisette J., Kretzschmar J., Haendler B., El-Hayek R.,
RA Mochena-Morales J., Martin B.M., Patel J.R., Moss R.L.,
RA Schlenker W.-D., Coronado R., Possani L.D.;
RT "Primary structure and properties of heliothermine, a peptide toxin
RT that blocks ryanodine receptors.";
RL Biophys. J. 68:2280-2288(1995).
RN [2]
RP SEQUENCE OF 20-39, AND CHARACTERIZATION.
RC TISSUE-Venom;
RX MEDLINE-90260878; PubMed-1693019;
RA Mochena-Morales J., Martin B.M., Possani L.D.;
RT "Isolation and characterization of heliothermine, a novel toxin from
RT Heloderma horridum horridum (Mexican beaded lizard) venom.";
RL Toxicon 28:299-309(1990).
CC -1- FUNCTION: Toxin that blocks ryanodine receptors. It is toxic to
CC mice; it causes lethargy, partial paralysis of rear limbs and
CC lowering of body temperature.
CC -1- TISSUE SPECIFICITY: Produced by the venomous gland.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC
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CC
DB EMBL; U13619; AAC59730.1; -
DR InterPro; IP0001283; Allrgn_V5/TPX1.
DR Pfam; PF00188; SCP.1.
DR PRINTS; PR00837; V5TPXLIKE.
DR PRODOM; PD000542; Allrgn_V5/TPX1.1.
DR SMART; SM00198; SCP.1.
DR PROSITE; PS01009; SCP_AGS_PRL_SCP_1.1.
DR PROSITE; PS01010; SCP_AGS_PRL_SCP_2.1.
KW Calcium channel inhibitor; Neurotoxin; Toxin; Signal.
FT SIGNAL 1 19
FT CHAIN 20 242
SO SEQUENCE 242 AA; 27493 MW; 0E183FC2925DF3C CRC64;

Query Match 13.8%; Score 137.5; DB 1; Length 242;

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Best Local Similarity 27.6%; Pred. No. 2,7e-05;
Matches 51; Conservative 23; Mismatches 72; Indels 39; Gaps 11;

OY 16 DAREEPEFHNGYRAAFANAYNTSKRMFMVDCITLSEKAYSAECS-EPSPSEENDV- 73
DB 34 DQGFETIDKHNRIARVEET--ASIMLKMTWNSKKNKINQNRANNCITLHSTKEETIDG 91
OY 74 -----VESNA--TLNITLEGNSSWMESEIFELRGKAYKNKNSITSN-----ANMYWDSH 119
DB 92 VECGSENFSSARPTYSVALQ---NMEDERRKTR--FPIGTAONVIGHYQVWYNS 145
OY 120 DNLGCAVYDC-----SKRTYVVCQ--GPEAKGDKITIEEGAPCSGSDYGAQVTCDDW 173
DB 146 YELGCAALNYCDPQPTKYIQVCQYCGGINSRKRTPYSIGPPCCDCPD-----ACD--- 197
OY 174 ONMLC 178
DB 198 -NGLC 201

RESULT 4
TPX1_HUMAN STANDARD; PRT; 243 AA.
ID TPX1_HUMAN
AC P16562;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Testis-specific protein TPX-1 precursor (cysteine-rich secretory
DE protein-2) (Crisp-2).
GN TPX1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid-9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Testis;
RX MEDLINE-90129048; PubMed-2613236;
RA Keshavarz M, Gutknecht J., Brew K., Spurr N., Goodfellow P.N.;
RT Cloning and mapping of a testis-specific gene with sequence
RT similarity to a sperm-coating glycoprotein gene.";
RL Genomics 3:527-534(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Testis;
RX MEDLINE-96270732; PubMed-8665901;
RA Knaetzschmar J., Haendler B., Eberspacher U., Roostermann D.,
RA Donner P., Schlömann W.-D.;
RT The human cysteine-rich secretory protein (CRISP) family. Primary
RT structure and tissue distribution of CRISP-1, CRISP-2 and CRISP-3.";
RL Eur. J. Biochem. 236:827-836(1996).
RN [3]
RP SUBCELLULAR LOCATION: Secreted (Probable).
CC -1- TISSUE SPECIFICITY: TESTIS AND EPIDIDYMIS.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC -----
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CC -----
DB EMBL: M25532; AAA61220.1; -
DB EMBL: X65239; CA64526.1; -
DB PIR: B33329; B33329.
DB Gene: HGNC:12024; TPX1.
DB MIM: 167430.
DB InterPro: IPR001283; Allrgn_V5/TPX1.
DB Pfam: PF00186; SCP.1.
DB PRINTS: PR00837; V5TPXLIKE.
DB ProDom: PD000543; Allrgn_V5/TPX1; 1.

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DR SMART: SM00198: SCP: 1.
DR PROSITE: PS01009: SCP_AGS_PRL_SC7.1: 1.
DR PROSITE: PS01010: SCP_AGS_PRL_SC7.2: 1.
KW Testis; Signal; Multigene family
FT SIGNAL 1 21
FT CHAIN 22 243 POTENTIAL
SO SEQUENCE 243 AA; 27259 MW; C5FE698C4ACAFD9 CRC64;

Query Match 13.78; Score 137; DB 1; Length 243;
Best Local Similarity 26.58; Pred. 3e-05;
Matches 49; Conservative 28; Mismatches 72; Indels 36; Gaps 9.

OY 18 REMETELHNGRAAFARANKYTSKMKTYVDCITLEEKYASAKESCEPSEEBE-----70
DB 38 RIIVYK-HNELRAAVSP--PAENMLKEMSERETTVAQMAWAKCTLIHSDPEDKYSTRC 94
OY 71 NYDVFSAATINIDPLENGSMWSEIFELRGKRYNKNKTSN-----IANYWSDHRLGCA 125
DB 95 GENLYMSDPTSSMSIAQEWDEILDF---YVGVGKSPNAVAGHYQLWVSTYGVGCG 151
OY 126 VYDC-----SGRTYVQYQYPEAKGDGK--TYEGAPCRSCSDYAGATCDD-----D 172
DB 153 IAYCNODSLKYYVQYQYCPAGNMNKRNPYQGGTPCAGCPD-----DCDKGLCTNSCQ 206
OY 173 WQMLL 177
DB 207 YQDLL 211

RESULT 5
CRS3_HUMAN
ID CRS3_HUMAN STANDARD; PRT: 245 AA.
AC P54108; O15512;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cysteine-rich secretory protein-3 precursor (CRISP-3) (SGP28 protein).
GN CRISP3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID:9606;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE-96770732; PubMed-8665901;
RA Kraetzschmar J., Haendler B., Eberspaecher U., Roostermann D.,
RA Donner P., Schleuning W.-D.;
RT "The human cysteine-rich secretory protein (CRISP) family. Primary
RT structure and tissue distribution of CRISP-1, CRISP-2 and CRISP-3.";
RL Eur. J. Biochem. 236:827-836(1996).
RN 12
RP SEQUENCE FROM N.A.
RX MEDLINE-96186934; PubMed-8601434;
RA Kjeldsen L., Cowland J.B., Johnson A.H., Borregaard N.;
RT "SGP28, a novel matrix glycoprotein in specific granules of human
RT neutrophils with similarity to a human testis-specific gene product
RT and a rodent sperm-coating glycoprotein.";
RL FEBS Lett. 380:246-250(1996).
CC -1- SUBCELLULAR LOCATION: SECRETED; IN NEUTROPHILS, LOCALIZED IN
CC SPECIFIC GRANULES.
CC -1- TISSUE SPECIFICITY: SALIVARY GLAND, PANCREAS AND PROSTATE >
CC EPIDIDYMIS, OVARY, THYMUS AND COLON.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SCT/SC14 AND PLANTS PR-1.
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EMBL: X95240; CAA64527.1; -  
 DR EMBL: X94323; CAA63984.1; -  
 DR HSSP: P04284; 1CFE.  
 DR InterPro: IPR001283; Allrgn\_V5/Tpx1.  
 DR Pfam: PF00188; SCP\_1.  
 DR PRINTS: PR00837; V5TPXLIKE.  
 DR PRODOM: PD000542; Allrgn\_V5/Tpx1; 1.  
 DR SMART: SM00198; SCP\_1.  
 DR PROSITE: PS01009; SCP\_A65\_PRL\_SCP\_1; 1.  
 DR PROSITE: PS01010; SCP\_A65\_PRL\_SCP\_2; 1.  
 DR Glycoprotein; Signal; Multigene family; Polymorphism.  
 KM SIGNAL 1 20  
 FT CHAIN 21 245 POTENTIAL.  
 FT CARBOHYD 239 239 N-LINKED (GLCNAC:...) (POTENTIAL).  
 FT VARIANT 106 106 S->P (IN DBSNP:495335).  
 FT VARIANT 134 134 A->S (IN DBSNP:1864312).  
 FT SIGNAL 1 22  
 FT CHAIN 23 243 TESTIS-SPECIFIC PROTEIN TPX-1.  
 SQ SEQUENCE 245 AA; 27630 MW; 6ADD79CB7AE9E5F9 CRC64;  
 Query Match 13.5%; Score 135; DB 1; Length 245;  
 Best Local Similarity 25.1%; Pred. No. 4,6e-05;  
 Matches 48; Conservative 23; Mismatches 76; Indels 44; Gaps 8;  
 QY 14 DDDKREKTEL-----HNGYRAAF---ARNTKSKRMVYDCTLEKAYK 56  
 DB 21 NEDDPFALLTQTQYQREIVKHNELRRSV---MLKMNKEAANAK 75  
 QY 57 SAERKSESEENVDFSAATLNIPLEAGNSMSEIFELRGVYKN-----KNG 106  
 DB 76 WANQCNVRHSNPKRDMNTSLKCGE-NLYMSASSMSQAQISMPEDYDFGVGPKTPVA 134  
 QY 107 KTSINAMVWDSHDKGCAVVDGSG---KTHVYCGYGEAKGSGKTI--YEEGACSCSC 160  
 DB 135 VVGHYGVVWSSYLVGSGNAYCQNVKLVKYYVCGYCPAGNMANRLVYVEGACACSC 194  
 QY 161 SDYGAGVTGDD 171  
 DB 195 PD-----NCDD 200

RESULT 6  
 TPX1\_MOUSE  
 ID TPX1\_MOUSE STANDARD; PRT; 243 AA.  
 AC P16563;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE Testis-specific protein TPX-1 precursor.  
 GN TPX1 OR TPX-1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Testis;  
 RX MEDLINE=90129048; PubMed=261336;  
 RA Kasahara M., Gutknecht J., Brew K., Spurr N., Goodfellow P.N.;  
 RT Cloning and mapping of a testis-specific gene with sequence  
 RT similarity to a sperm-coating glycoprotein gene.\*  
 RL Genomics 5:527-534(1989).  
 CC -1- SUBCELLULAR LOCATION: Secreted (Probable).  
 CC -1- TISSUE SPECIFICITY: TESTIS.  
 CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;  
 CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1  
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 CC EMBL: M25533; AAA40472.1; -  
 DR EMBL: A33329; A33329.  
 DR HSSP: P04284; 1CFE.  
 DR MGD: MGI:98815; Tpx1.  
 DR InterPro: IPR001283; Allrgn\_V5/Tpx1.  
 DR Pfam: PF00188; SCP\_1.  
 DR PRINTS: PR00837; V5TPXLIKE.  
 DR PRODOM: PD000542; Allrgn\_V5/Tpx1; 1.  
 DR SMART: SM00198; SCP\_1.  
 DR PROSITE: PS01009; SCP\_A65\_PRL\_SCP\_1; 1.  
 DR PROSITE: PS01010; SCP\_A65\_PRL\_SCP\_2; 1.  
 DR Testis; Signal.  
 KM SIGNAL 1 22  
 FT CHAIN 23 243 TESTIS-SPECIFIC PROTEIN TPX-1.  
 SQ SEQUENCE 243 AA; 27605 MW; 6E707F569ACAA244 CRC64;  
 Query Match 12.7%; Score 127; DB 1; Length 243;  
 Best Local Similarity 24.9%; Pred. No. 0.00024;  
 Matches 49; Conservative 28; Mismatches 84; Indels 36; Gaps 9;  
 QY 11 EKLDMDREMT-----ELNNGYRAAFARNYKTSKRTMYDCTLEKAYKSAEK 60  
 DB 21 EGKDDPFTSLTQYQREIVKHNELRRSV---NPTGSDILKMSIQATTNQKANK 78  
 QY 61 CSEPSSEENVDFSAATLNIPLEAGNSMSEIFELRGVYKN-----GKTSNIA- 112  
 DB 79 CILHSSADR-KINIRCGENLYMSTDTLWSTVIG---SWNENEDFYVGAKPNSAV 134  
 QY 113 ----NMVWDSHDKGCAVVDGSGKTHV---VCOYGEAKGSGKTI--YEEGACSCSC 162  
 DB 135 GHYTLVWSSYLVGSGNAYCQNVKLVKYYVCGYCPAGNMANRLVYVEGACACSC 194  
 QY 163 YGAGVTGDD--DQNTLL 177  
 DB 195 NCENGLCTNSCFEDLL 211

RESULT 7  
 VAS3\_POLDO  
 ID VAS3\_POLDO STANDARD; PRT; 206 AA.  
 AC P81656;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Venom allergen 5 (Antigen 5) (AG5) (Allergen Pol d 5).  
 OS Polistes dominulus (European paper wasp).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;  
 OC Aculeata; Vespidae; Vespidae; Polistinae; Polistes.  
 OX NCBI\_TaxID=34728;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RA Hoffman D.R.;  
 RL Submitted (FEB-1999) to the SWISS-PROT data bank.  
 CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;  
 CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.  
 DR HSSP: P04284; 1CFE.  
 DR InterPro: IPR001283; Allrgn\_V5/Tpx1.  
 DR Pfam: PF00188; SCP\_1.  
 DR PRINTS: PR00837; V5TPXLIKE.  
 DR PRODOM: PD000542; Allrgn\_V5/Tpx1; 1.  
 DR SMART: SM00198; SCP\_1.  
 DR PROSITE: PS01009; SCP\_A65\_PRL\_SCP\_1; 1.  
 DR PROSITE: PS01010; SCP\_A65\_PRL\_SCP\_2; 1.  
 DR Venom; Allergen.  
 KM DISULFID 6 16  
 FT DISULFID 8 104 BY SIMILARITY.  
 FT DISULFID 28 96 BY SIMILARITY.  
 FT DISULFID 112 189 BY SIMILARITY.  
 SQ SEQUENCE 206 AA; 23152 MW; 2E525705A7875DA8 CRC64;



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CC DUCTUS DEFERENS.
CC -1 SUBCELLULAR LOCATION: STORED IN SECRETORY GRANULES OF GRANULAR
CC CONVOLUTED TUBULES CELLS.
CC -1 TISSUE SPECIFICITY: MAINLY FOUND IN THE CAUDA EPIDIDYMAIS WHERE IT
CC IS SYNTHESIZED BY THE PRINCIPAL CELLS AND SECRETED INTO THE LUMEN.
CC BINDS TO THE HEADS OF SPERMATOZOA. ALSO EXPRESSED IN THE
CC SUBMANDIBULAR GLAND.
CC -1 DEVELOPMENTAL STAGE: EXPONENTIAL INCREASE BETWEEN DAYS 25 AND 30
CC AFTER BIRTH.
CC -1 INDUCTION: By androgens.
CC -1 SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC -----
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CC or send an email to license@sdb.sdb.ch).
CC -----
DR EMBL: M92849; AAA37185.1; -
DR EMBL: L05559; AAA37460.1; -
DR PIR: A49202; A49202.
DR MGI: MGI:102553; Aeg1.
DR InterPro: IPR001283; Allrgn_V5/TPx1.
DR Pfam: PF00188; SCP; 1.
DR PRINTS: PR00837; V5TPXLIKE.
DR PRODOM: PD000542; Allrgn_V5/TPx1; 1.
DR SMART: SM00198; SCP; 1.
DR PROSITE: PS01009; SCP_AGS_PRI_SC7_1; 1.
DR PROSITE: PS01010; SCP_AGS_PRI_SC7_2; 1.
DR KEGG: Glycopolin; Signal.
DR SIGNAL: 1
DR CHAIN: 19
DR CARBOHYD: 20 244 N-LINKED (GLCNAC...) (POTENTIAL).
DR FT SEQUENCE 244 AA; 27679 MW; D0DD0348B857B1F CRC64;
SQ
Query Match 12.0%; Score 119.5; DB 1; Length 244;
Best Local Similarity 25.4%; Pred. No. 0.0011;
Matches 51; Conservative 31; Mismatches 84; Indels 35; Gaps 10;
OY 3 DYSICQREKLD--DMREMFELHNGYRAFAFANKYTKSMRTVYDCTLEKAYKSAE 59
DB 21 DSSQENRELEKLTSTRMSVQOEIVSKHQLRRVSPS--GSLKMKEMNYDAQVNAQWAD 78
OY 60 KCSEPSSE-----ENVDFSAATLNPLEAGNSMSEIFELRGKYNK--NGKT 108
DB 79 KCFSSHPELERTNLTNRGEN--LFMSVYLAQMSALQGYNYEXDLYDVGPRQPSVY 136
OY 109 SNIAHWYDSDHDKGCAVYDCSG--KTHVCGYGPPEAKGDGK--TITEEGAPGCRSDY 163
DB 137 GHYGVNMSSTFOVACVACPKNPRYYVCHICPYGNTGSLYTPYTAGERPCASCPDH 196
OY 164 GAGVCCDDMNILC-----IGH 181
DB 197 -----CEDG-----LCITNSCGH 208

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RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE-VENOM;
RX MEDLINE-88124947; Pubmed-3422469;
RA Fang K.S.Y., Vitale M., Fehlner P., King T.P.;
RT cDNA cloning and primary structure of a white-face hornet venom
RN allergen, antigen 5.
RN Proc. Natl. Acad. Sci. U.S.A. 85:895-899(1988).
RP PARTIAL SEQUENCE, AND DISULFIDE BONDS.
RC TISSUE-Venom;
RX MEDLINE-90384920; Pubmed-2402482;
RA King T.P., Moran D., Wang D.F., Kochoomian L., Chalt B.T.;
RT Structural studies of a hornet venom allergen antigen 5, Dol m v and
RT its sequence similarity with other proteins.
RT Protein Seq. Data Anal. 3:263-266(1990).
CC -1 SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC -----
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CC entities requires a license agreement (See http://www.isb-sdb.ch/announce/
CC or send an email to license@sdb.sdb.ch).
CC -----
DR EMBL: J03601; AAA28301.1; -
DR PIR: A31085; A31085.
DR HSSP: P04284; ICEE.
DR InterPro: IPR001283; Allrgn_V5/TPx1.
DR Pfam: PF00188; SCP; 1.
DR PRINTS: PR00837; V5TPXLIKE.
DR PRODOM: PD000542; Allrgn_V5/TPx1; 1.
DR SMART: SM00198; SCP; 1.
DR PROSITE: PS01009; SCP_AGS_PRI_SC7_1; 1.
DR PROSITE: PS01010; SCP_AGS_PRI_SC7_2; 1.
DR KEGG: Allergen; Signal; Multigene family.
DR SIGNAL: 1
DR CHAIN: 23
DR FT CHAIN 24 227 VENOM ALLERGEN 5.01.
DR FT DISULFID 27 39
DR FT DISULFID 31 124
DR FT DISULFID 49 117
DR FT DISULFID 193 210
DR FT VARIANT 54 54 V -> A.
DR SEQUENCE 227 AA; 25999 MW; 4F0ED10D58C44502 CRC64;
SQ
Query Match 11.3%; Score 112.5; DB 1; Length 227;
Best Local Similarity 23.4%; Pred. No. 0.0043;
Matches 39; Conservative 27; Mismatches 74; Indels 27; Gaps 6;
OY 13 LDDMRREMFELHNGYRAFAFANKYTKSMRTVYDCTLEKAYKSAEKC- 61
DB 59 LNDENKEILAKRNDPRNVAKCLETGRKGPQPRPAKNMNLVWDELAKIATYANQCD 118
OY 62 -----SEEPSSEENDVFS--AATLNPLEAGNSMSEIFELRGKYNK--KTS 109
DB 119 FPHDDCRNTAKYGVGNINISSTRTQFDPKSLIKQWEDVETENKIKVLGNSNRRKVG 178
OY 110 NIAHWYDSDHDKGCA--VYDCSGKTH--VYCOYGPPEAKGDGKTYTE 152
DB 179 HITQWVGKTKETIGCGSIXITIEDMNTHTLVLCNIGGNDENQPIYE 225

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RESULT 10
V552.DOLMA STANDARD: PRT: 227 AA.
AC P10735;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Venom allergen 5, 01 precursor (antigen 5 form 2) (AG5-2) (Allergen Dol
m 5.01) (Dol m V-A).
OS Dolichovespula maculata (White-face hornet) (Bald-faced hornet).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC Aculeata; Vespidae; Vespinae; Dolichovespula.
NCBI_TaxID=7441;

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RESULT 11
V45.VESGE STANDARD: PRT: 204 AA.
AC P35784;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Venom allergen 5 (antigen 5) (AG5) (Allergen Ves g 5) (Ves g V).
OS Vespula germanica (yellow jacket) (Wasp).

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OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC Aculeata; Vespoidea; Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=30212;
RM [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=94044316; PubMed=8227862;
RA Hoffman D.R.;
RT "Allergens in Hymenoptera venom. XXV: The amino acid sequences of
RT antigen 5 molecules and the structural basis of antigenic cross-
RT reactivity."
RL J. Allergy Clin. Immunol. 92:707-716(1993).
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC PIR; H44522; H44522.
CC PIR; H44583; H44583.
CC HSSP; P04284; ICFE.
CC InterPro; IPR001283; Allrgn_V5/TPx1.
CC Pfam; PF00188; SCP; 1.
CC PRINTS; PR00837; V5TPXLIKE.
CC PRODOM; PD000542; Allrgn_V5/TPx1; 1.
CC SMART; SM00198; SCP; 1.
CC PROSITE; PS01009; SCP_AG5_PRL_SC7_1; 1.
CC PROSITE; PS01010; SCP_AG5_PRL_SC7_2; 1.
CC Venom; Allergen.
KW Venom; Allergen.
FT DISULFID 4 17 BY SIMILARITY.
FT DISULFID 8 101 BY SIMILARITY.
FT DISULFID 26 94 BY SIMILARITY.
FT DISULFID 170 187 BY SIMILARITY.
SQ SEQUENCE 204 AA; 23330 MW; DIFB4BD21C7BCE CRC64;

Query Match 11.2%; Score 112; DB 1; Length 204;
Best local similarity 22.2%; Pred. No. 0.0042;
Matches 39; Conservative 34; Mismatches 69; Indels 34; Gaps 7;

OY 4 YELCOGRKLDHDDREKFTLHNGRAAFANRYT-----SKRTMYVDTCTLEEK 53
ID TPX1_CAVPO STANDARD; PRT; 202 AA.
AC P35782;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Venom allergen 5.02 (Antigen 5-2) (AG5-2) (Allergen Vesp c 5.02) (Vesp
DE C.V.02).
OS Vespa crabro (European hornet).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC Aculeata; Vespoidea; Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=7445;
RM [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=94044316; PubMed=8227862;
RA Hoffman D.R.;
RT "Allergens in Hymenoptera venom. XXV: The amino acid sequences of
RT antigen 5 molecules and the structural basis of antigenic cross-
RT reactivity."
RL J. Allergy Clin. Immunol. 92:707-716(1993).
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;

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CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC PIR; H44522; H44522.
CC PIR; H44583; H44583.
CC HSSP; P04284; ICFE.
CC InterPro; IPR001283; Allrgn_V5/TPx1.
CC Pfam; PF00188; SCP; 1.
CC PRINTS; PR00837; V5TPXLIKE.
CC PRODOM; PD000542; Allrgn_V5/TPx1; 1.
CC SMART; SM00198; SCP; 1.
CC PROSITE; PS01009; SCP_AG5_PRL_SC7_1; 1.
CC PROSITE; PS01010; SCP_AG5_PRL_SC7_2; 1.
CC Venom; Allergen.
KW Venom; Allergen.
FT DISULFID 4 16 BY SIMILARITY.
FT DISULFID 8 101 BY SIMILARITY.
FT DISULFID 26 94 BY SIMILARITY.
FT DISULFID 168 185 BY SIMILARITY.
SQ SEQUENCE 202 AA; 22781 MW; B710E9198413F547 CRC64;

Query Match 11.2%; Score 111.5; DB 1; Length 202;
Best local similarity 22.8%; Pred. No. 0.0046;
Matches 37; Conservative 24; Mismatches 58; Indels 43; Gaps 5;

OY 25 HNGRYAFAFANRYT-----SKRTMYVDTCTLEEKAKSAKRC----- 61
ID TPX1_CAVPO STANDARD; PRT; 244 AA.
AC Q60477;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Testis-specific protein Tpx-1 precursor (Autoantigen 1) (25 kDa
DE acrosomal autoantigen) (AA1).
GN TPX1.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognath; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RM [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Hartley; TISSUE=Testis;
RX MEDLINE=96354287; PubMed=9115720;
RA Foster J.A.; Gerton G.L.;
RT "Autoantigen 1 of the guinea pig sperm acrosome is the homologue of
RT mouse Tpx-1 and human TPX1 and is a member of the cysteine-rich
RT secretory protein (CRISP) family."
RL Mol. Reprod. Dev. 44:221-229(1996).
RN [2]
RP SEQUENCE OF 22-41.
RX MEDLINE=88193219; PubMed=328255;
RA Hardy D.M.; Huang T.T.F.; Jr.; Driscoll W.J.; Tung K.S.K.; Wild G.C.;
RT "Purification and characterization of the primary acrosomal
RT autoantigen of guinea pig epididymal spermatozoa."
RL Biol. Reprod. 38:423-437(1988).
CC -1- TISSUE SPECIFICITY: TESTIS.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
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Db 161 MWAKTEKIGGSGSJKRYKVDNNHTHYLVANCYGPAPAGNENGDEYTE 203
|||||
RESULT 16
VA53_DOLMA STANDARD; PRT; 215 AA.
ID VA53_DOLMA
AC PI0737;
DR 01-JUN-1989 (Rel. 11, Created)
DR 01-JUN-1994 (Rel. 29, Last sequence update)
DR 01-NOV-1997 (Rel. 35, Last annotation update)
DE Venom allergen 5.02 precursor (Antigen 5 form 3) (AG5-3) (Allergen Dol
m 5.02) (Dol m V-B) (fragment).
OS Dolichovespula maculata (White-face hornet) (Bald-faced hornet).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
Aculeata; Vespoidae; Vespidae; Vespinae; Dolichovespula.
NA K05L1;taxid=7441;
(1)
DR NM
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RP TISSUE-Venom;
RA MEDLINE=891324947; PubMed=3422469;
RA Fang K.S.Y., Vitale M., Fehner P., King T.P.;
RT "DNA cloning and primary structure of a white-face hornet venom
allergen, antigen 5."
RT Proc. Natl. Acad. Sci. U.S.A. 85:895-899(1988).
(2)
DR NM
RP PARTIAL SEQUENCE, AND DISULFIDE BONDS.
RP TISSUE-Venom;
RA MEDLINE=903846920; PubMed=2402482;
RA King T.P., Moran D., Wang D.F., Kochoyuan L., Chait B.T.;
RT "Structural studies of a hornet venom allergen antigen 5, Dol m V and
its sequence similarity with other proteins."
RT Protein Seq. Data Anal. 3:263-266(1990).
(1) SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCF/TPX1;
INSCPTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC CC
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL J03602; AAA28302.1; ALT-TERM.
DR PIR; B31085; B31085.
DR InterPro; IPR001283; Allrgn_V5/Tpx1.
DR Pfam; PF00186; SCP.1.
DR ProDom; PDO00542; Allrgn_V5/Tpx1; 1.
DR SMART; SM00198; SCP.1.
DR PROSITE; PS01009; SCP_AGS_PRL_SCF.1; 1.
DR PROSITE; PS01010; SCP_AGS_PRL_SCF.2; 1.
KW Venom; Allergen; Signal; Multigene family.
FT NON_TER 1
FT SIGNAL 1
FT CHAIN 11 10 VENOM ALLERGEN 5.02.
FT DISULFID 11 215
FT DISULFID 14 26
FT DISULFID 18 111
FT DISULFID 36 104
FT DISULFID 181 198
SQ SEQUENCE 215 AA; 24270 MW; DPEPEB99CE9AOBA CRC64;

Query Match 10.8%; Score 108; DB 1; Length 215;
Best local Similarity 23.4%; Pseq. NO. 0.01;
Matches 40; Conservative 30; Mismatches 67; Indels 34; Gaps 8;

07 13 LDDDMRELFELNGRAAFANRYT-----SKRTMYQCTLEAKYKSKES 62
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 46 VDNDEKNEIYNRNHGRKQVAGLETRNGNPPPPAKNNAYLVNMDLAKTQATWAKQCS 105
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
07 63 -----EPPSSEENDVYSA-----ATLNTPLDAGSWSSETEFE--RKQVYNNK- 105
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |

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[illegible]

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VA5_VESMC STANDARD; PRT: 204 AA.
ID VAS1_VESMC
AC P35760;
RT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DE 01-NOV-1997 (Rel. 35, Last annotation update)
OS Venom allergen 5 (Antigen 5) (AG5) (Allergen Ves m 5) (Ves m V).
OC Vesputia maculifrons (Eastern yellow jacket) (Wasp).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC Aculeata; Vespoidea; Vespidae; Vespinae; Vespula.
OX NCBI_TaxID=7453;
RN [1]
RP SEQUENCE.
RC MEDLINE=93203603; PubMed=8454859;
RA La G., Villalba M., Coscia M.R., Hoffman D.R., King T.P.;
RT "Sequence analysis and antigenic cross-reactivity of a venom
allergen, antigen 5, from hornets, wasps, and yellow jackets."
RL J. Immunol. 150:2823-2830(1993).
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
DR PIR: B37329; B37329.
DR HSSP: P04284; ICPE.
DR InterPro: IPR001283; Allrgn_V5/TPx1.
DR Pfam: PF00188; SCP. 1.
DR PRINTS: PR00837; V5TPXLIKE.
DR PRODOM: PD000542; Allrgn_V5/TPx1; 1.
DR SMART: SM00198; SCP. 1.
DR PROSITE: PS01009; SCP_AGS_Prl_Sc7_1; 1.
DR PROSITE: PS01010; SCP_AGS_Prl_Sc7_2; 1.
KM Venom; Allergen.
FT DISULFID 4 17 BY SIMILARITY.
FT DISULFID 8 101 BY SIMILARITY.
FT DISULFID 26 94 BY SIMILARITY.
FT DISULFID 170 187 BY SIMILARITY.
SQ SEQUENCE 204 AA; 23332 MW; 8B68A94C1390311 CRC64;

Query Match 10.6%; Score 107; DB 1; Length 204;
Best Local Similarity 21.6%; Pred. No. 0.012; Mismatches 34; Gaps 7;
Matches 38; Conservative 34; Indels 34;

QY 4 YSLCQREKLDMDREMTFELHNGYRAAFARNTK-----SKMRTVYDCGLEEK 53
ID VAS1_VESMC STANDARD; PRT: 204 AA.
AC P35783;
RT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DE 01-NOV-1997 (Rel. 35, Last annotation update)
OS Venom allergen 5 (Antigen 5) (AG5) (Allergen Ves f 5) (Ves f V).
OC Vesputia flavopilosa (Yellow jacket) (Wasp).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC Aculeata; Vespoidea; Vespidae; Vespinae; Vespula.
OX NCBI_TaxID=30211;
RN [1]
RP SPOUNCE.
RC MEDLINE=94044316; PubMed=8227862;
RA Hoffman D.R.;

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RT "Allergens in Hymenoptera venom. XXV: The amino acid sequences of
antigen 5 molecules and the structural basis of antigenic cross-
reactivity."
RL J. Allergy Clin. Immunol. 92:707-716(1993).
CC -1- FUNCTION: MAY HAVE AN ANCESTRAL FUNCTION IN THE PROMOTION OF
OVUM FERTILIZATION BY Sperm.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
DR PIR: B44522; B44522.
DR PIR: A44583; A44583.
DR HSSP: P04284; ICPE.
DR InterPro: IPR001283; Allrgn_V5/TPx1.
DR Pfam: PF00188; SCP. 1.
DR PRINTS: PR00837; V5TPXLIKE.
DR PRODOM: PD000542; Allrgn_V5/TPx1; 1.
DR SMART: SM00198; SCP. 1.
DR PROSITE: PS01009; SCP_AGS_Prl_Sc7_1; 1.
DR PROSITE: PS01010; SCP_AGS_Prl_Sc7_2; 1.
KM Venom; Allergen.
FT DISULFID 4 17 BY SIMILARITY.
FT DISULFID 8 101 BY SIMILARITY.
FT DISULFID 26 94 BY SIMILARITY.
FT DISULFID 170 187 BY SIMILARITY.
SQ SEQUENCE 204 AA; 23274 MW; 7667232536A32F5 CRC64;

Query Match 10.6%; Score 106; DB 1; Length 204;
Best Local Similarity 21.6%; Pred. No. 0.014; Mismatches 38; Conservative 35; Indels 34; Gaps 7;
Matches 38; Conservative 35; Mismatches 69; Indels 34;

QY 4 YSLCQREKLDMDREMTFELHNGYRAAFARNTK-----SKMRTVYDCGLEEK 53
ID VAS1_VESCR STANDARD; PRT: 202 AA.
AC P35781;
RT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
OS Venom allergen 5.01 (Antigen 5-1) (AG5-1) (Allergen Ves c 5.01) (Ves
c V.01).
DE Vespa c.01 (European hornet).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC Aculeata; Vespoidea; Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=7445;
RN [1]
RP SEQUENCE.
RC MEDLINE=94044316; PubMed=8227862;
RA Hoffman D.R.;
RT "Allergens in Hymenoptera venom. XXV: The amino acid sequences of
antigen 5 molecules and the structural basis of antigenic cross-
reactivity."
RL J. Allergy Clin. Immunol. 92:707-716(1993).
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
DR PIR: G44522; G44522.
DR PIR: G44583; G44583.
DR HSSP: P04284; ICPE.
DR InterPro: IPR001283; Allrgn_V5/TPx1.
DR Pfam: PF00188; SCP. 1.
DR PRINTS: PR00837; V5TPXLIKE.

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DR PRODOM: PD000542; Allrgn\_V5/Tpx1; 1.  
 DR SMART: SM00198; SCP; 1.  
 DR PROSITE: PS01009; SCP\_AGS\_PRI\_SCP\_1; 1.  
 DR PROSITE: PS01010; SCP\_AGS\_PRI\_SCP\_2; 1.  
 KW Venom: Allergen.  
 FT DISULFID 4 16 BY SIMILARITY.  
 FT DISULFID 8 101 BY SIMILARITY.  
 FT DISULFID 26 94 BY SIMILARITY.  
 FT DISULFID 168 185 BY SIMILARITY.  
 SQ SEQUENCE 202 AA; 22722 MW; EDEB399058598997 CRC64;  
 Query Match 10.6%; Score 105.5; DB 1; Length 202;  
 Best Local Similarity 22.2%; Pred. No. 0.016;  
 Matches 35; Conservative 26; Mismatches 62; Indels 35; Gaps 6;  
 QY 25 HNGYRAAFARNTKT-----SKRTMYDCTLEKAKYSAKCS-----62  
 DB 48 HNEFRKXVARGLETGNPGPPAKKMTLVNDELAIQVMAVANCNGHDCNSAKY 107  
 QY 63 --EEPSSEENVDFSAATLNIPLEAGNSWSEIFELR-GKYVKNKGTSTIANVWDS 118  
 DB 108 SVGQNTAEGSTADPFGSVSNVWK-----WDEKQDYQSPKNTKRGHTQVWAK 162  
 QY 119 HDRLGCAVDC--SG--KTHVCCQYGPBAGKDGKTYE 152  
 DB 163 TKEIGSGSTIKYIENGHRHRYLVCNYPGAGVNGEPIYE 200  
 RESULT 21  
 ID YRBL\_CAEEL STANDARD: PRT; 312 AA.  
 AC 009366; 1997 (rel. 35; Created).  
 DT 01-NOV-1997 (rel. 35; Last sequence update).  
 DT 16-NOV-2001 (rel. 40; Last annotation update).  
 DR 16-HCT-2001 (rel. 40; Last annotation update).  
 DR Hypothetical 35.0 kDa protein F48E8.1 in chromosome III.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromodorea; Rhabditidae; Rhabditoidae;  
 OC Rhabditidae; Polodierinae; Caenorhabditis.  
 NCBI\_TaxID=6239;  
 RN NCBI\_TaxID=6239;  
 RM SEQUENCE FROM N.A.  
 RC STRAIN-Bristol N2;  
 RA Kirsten J.;  
 RT Submitted (MAR-1995) to the EMBL/Genbank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;  
 CC -1- INSECTS AG3/AG5; FUNGI SCT/SC14 AND PLANTS PR-1.  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC EMBL: U23514; AAC46538.1;  
 DR WormPep; F48E8.1; CE01953.  
 DR InterPro: IPR001283; Allrgn\_V5/Tpx1.  
 DR Pfam: PF00188; SCP; 1.  
 DR PRINTS: PR00837; V5TPX1KE.  
 DR PRODOM: PD000542; Allrgn\_V5/Tpx1; 1.  
 DR SMART: SM00198; SCP; 1.  
 DR PROSITE: PS01009; SCP\_AGS\_PRI\_SCP\_1; FALSE\_NG.  
 DR PROSITE: PS01010; SCP\_AGS\_PRI\_SCP\_2; FALSE\_NG.  
 KW Hypothetical protein.  
 FT DOMAIN 265 268 POLY-THR.  
 FT DOMAIN 299 303 POLY-GLU.  
 SQ SEQUENCE 312 AA; 35054 MW; AEFCTBFF25E26288 CRC64;  
 Query Match 10.5%; Score 105; DB 1; Length 312;  
 Best Local Similarity 21.7%; Pred. No. 0.029;

Matches 41; Conservative 30; Mismatches 80; Indels 38; Gaps 8;  
 QY 1 EDDYSLCOQREKIDDMRMFTELNGYRAAFARNTKTMYDCTLEKAKYSAK 60  
 DB 64 QSDSGLSRSEHNEHLYKWTIHEHNR-----RMVPADDMNKLWSEDLAASQRIADT 119  
 QY 61 CSEEPSSEENV--DVFSATLNIPLEAGNSWSEIFELR-GKYVKNKGTSTIANVWDS 117  
 DB 120 CDFRSRGRINVENGTMAAPYSNYS-DAISITENEVHNPCCMNAHYHCCGHVQVWA 178  
 QY 118 SHDKLGCAVDCS-----GKTH--VYCCYGPBAGKDGKTYE 151  
 DB 179 KTNLVGCGFCFSDVGVGVRGRHNVFVCHYRPO---GNTVFYTAHQLYAMPAFTWAS 234  
 QY 152 EKGAPCSRC 160  
 DB 235 GDNGKCSMC 243  
 RESULT 22  
 ID VAS\_VESPE STANDARD: PRT; 204 AA.  
 AC P35785;  
 DT 01-JUN-1994 (rel. 28; Created).  
 DT 01-NOV-1997 (rel. 35; Last sequence update).  
 DT 01-NOV-1997 (rel. 35; Last annotation update).  
 DR Venom allergen 5 (Allergen 5) (AG5) (Allergen Yes p 5) (Yes p V).  
 OS Vespaula pensylvanica (Allergen yellow jacket) (Maep).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Vespaidea; Neoptera; Endopterygota; Hymenoptera; Apocrita;  
 OC NCBI\_TaxID=30213;  
 RN NCBI\_TaxID=30213;  
 RM SEQUENCE.  
 RC TISSUE-Venom;  
 RX MEDLINE=94044316; PubMed=8227862;  
 RA Hoffman D.R.;  
 RT "Allergens in Hymenoptera venom. XXV: The amino acid sequences of  
 RT antigen 5 molecules and the structural basis of antigenic cross-  
 RT reactivity".  
 RT J. Allergy Clin. Immunol. 92:707-716(1993).  
 CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;  
 CC -1- INSECTS AG3/AG5; FUNGI SCT/SC14 AND PLANTS PR-1.  
 CC PIR: C44522; C44522.  
 DR PIR: C44583; C44583.  
 DR HSSP: P04284; ICFE.  
 DR InterPro: IPR001283; Allrgn\_V5/Tpx1.  
 DR Pfam: PF00188; SCP; 1.  
 DR PRINTS: PR00837; V5TPX1KE.  
 DR PRODOM: PD000542; Allrgn\_V5/Tpx1; 1.  
 DR SMART: SM00198; SCP; 1.  
 DR PROSITE: PS01009; SCP\_AGS\_PRI\_SCP\_1; 1.  
 DR PROSITE: PS01010; SCP\_AGS\_PRI\_SCP\_2; 1.  
 KW Venom: Allergen.  
 FT DISULFID 4 17 BY SIMILARITY.  
 FT DISULFID 8 101 BY SIMILARITY.  
 FT DISULFID 26 94 BY SIMILARITY.  
 FT DISULFID 170 187 BY SIMILARITY.  
 SQ SEQUENCE 204 AA; 23317 MW; 85ED971066C/D7C8 CRC64;  
 Query Match 10.3%; Score 103; DB 1; Length 204;  
 Best Local Similarity 20.6%; Pred. No. 0.027;  
 Matches 35; Conservative 31; Mismatches 72; Indels 32; Gaps 5;  
 QY 10 REKLDDMREMFTELNGYRAAFARNTKT-----SKRTMYDCTLEKAKYSAK 59  
 DB 38 KEKKDILKE-----HDFRQKTARGLTGRNGPPAKKMTLVNDELAVYVQVWAN 92  
 QY 60 KC-----SEEPSSEENVDFSAATLNIPLEAGNSWSEIFELGK---VYKNG 106  
 DB 93 QCCYGHGHCQDVAKYATPGVAVNLGSGTADKTNPKVLYKMEDEVDVADYPAKKPSENN 152  
 QY 107 KTSNIANVWDSHDKLGCAVDCS-----GKTHVCCQYGPBAGKDGKTYE 152



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Db          153 KGHGTHVMANKTEIGCSIVYIONEMWHEKHVYLCNCGSPNGNEELYQ 202
          1 : 111 : 111 : 1 : 111 111
RESULT 23
ID ID VA5 VESVU STANDARD; PRT: 227 AA.
AC 005110; 090B91;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Venom allergen 5 precursor (Antigen 5) (AG5) (Allergen Ves v 5) (Ves v
DE V.)
DE Vesputia vulgaris (Yellow jacket) (Wasp).
DE Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
DE Insecta; Psterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
DE Aculeata; Vespoidea; Vespidae; Vespinae; Vespula.
OX NCBI_TaxID=7454;
RN 11
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Venom;
RC MEDLINE=93703603; Pubmed=8454859;
RA Lu G., Villalba M., Coscia M.R., Hoffman D.R., King T.P.;
RA "Antigen cloning of a genomic sequence from the venom allergen
RT allergen, antigen 5, from hornets, wasps, and yellow jackets."
RT J. Immunol. 150:2823-2830(1993).
RN 12
RP SEQUENCE OF 24-227 FROM N.A.
RA Suck R., Hegen S., Fiebig H.;
RA "Molecular cloning of a genomic sequence from the venom allergen
RT antigen 5 from Vespula vulgaris."
RT Submitted (May-1995) to the EMBL/Genbank/DBD databases.
RL 1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX;
CC INSECTS AG3/AG5; FUNGI SCT/SC14 AND PLANTS PR-1.
CC -----
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CC -----
DR EMBL; M98658; AA303033.1;
DR EMBL; A238849; CA842887.1;
DR HSSP; P04284; ICPE.
DR InterPro; IPR001283; Allrgn_V5/TPx1.
DR Pfam; PF00188; SCP.1.
DR PRINTS; PR00837; VSTPKLIRE.
DR ProDom; PD000542; Allrgn_V5/TPx1.1.
DR SMART; SM00198; SCP.1.
DR PROSITE; PS01009; SCP_AG5_Prl_Sc7_1; 1.
DR PROSITE; PS01010; SCP_AG5_Prl_Sc7_2; 1.
RV Venom; Allergen; signal.
FT FT SIGNAL 1 23
FT CHAIN 24 227
FT DISULEID 27 40 VENOM ALLERGEN 5.
FT DISULEID 31 124 BY SIMILARITY.
FT DISULEID 49 117 BY SIMILARITY.
FT DISULEID 193 210 BY SIMILARITY.
FT CONFLICT 109 109 V -> I (IN REF. 2).
FT CONFLICT 118 118 O -> E (IN REF. 2).
FT CONFLICT 173 173 D -> N (IN REF. 2).
FT CONFLICT 219 219 M -> K (IN REF. 2).
SQ SEQUENCE 227 AA; 25798 MW; 99998013740A6655 CRC64;
Best Match 10.38; Score 103; DB 1; Length 227;
Matches 39; Conservative 52; Pctid No. 0.03; Mismatches 66; Indels 44; Gaps 7
Oy 4 YSLCOQRERLDDDKREKFTELHNGRAFAFARKYT-----SKRTIVDTLKEK 53
Db 57 YGLTKQENQ-DLTK-----HNDKRLAIAGLETGKNGPQPPAKRNNKINLWMDLQY 109

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OY 54 YKFAEAC-----SEEPSSEENVDFEAFALINPLEAGSMWSSEIFELARKEYN 103
Db 110 AQWANQCOYGHDTCDYKAYQVGNALYNGSTAAKYDDPYALVYMEDRY-----KOYN 164
OY 104 KNG-----KTSNANWMDSHDYGCA-----VYDSCGRHHVCOYGEARKDGCKTY 151
Db 165 PKKFSNDPLKRGHTGTQWMAANKREVGCSIKYIDKMKHXYLVCNYSGFNFMEELY 224
OY 152 E 152
Db 225 Q 225

RESULT 24
AEG2_MOUSE
ID AEG2_MOUSE STANDARD; PRT: 241 AA.
AC Q03402;
DR 01-OCT-1993 (Rel. 27, Created)
DR 01-OCT-1993 (Rel. 27, Last sequence update)
DR 13-JUN-2002 (Rel. 41, Last annotation update)
DE Sperm-coating glycoprotein 2 precursor (SCP 2) (Acidic epididymal
DE glycoprotein 2) (Cysteine-rich secretory protein-3) (Crisp-3).
GN AEG2 OR AEG-2
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId:10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Submandibular gland;
RC MEDLINE=93246016; PubMed=1301383;
RA Mizuki N., Kasahara M.;
RT "Mouse submandibular glands express an androgen-regulated transcript
RT encoding an acidic epididymal glycoprotein-like molecule.";
RT Mol. Cell. Endocrinol. 89:25-32(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Submandibular gland;
RC MEDLINE=93307144; PubMed=8319566;
RA Heendler B., Kratzschmar J., Theuring F., Schlenning W.D.;
RT "Transcripts for cysteine-rich secretory protein-1 (CRISP-1; DE/AEG)
RT and the novel related CRISP-3 are expressed under androgen control in
RT the mouse salivary gland.";
RT Endocrinology 133:192-198(1993).
RC -1- FUNCTION: THIS PROTEIN IS SUPPOSED TO HELP SPERMATOZOA UNDERGO
CC FUNCTIONAL MATURATION WHILE THEY MOVE FROM THE TESTIS TO THE
CC DUCTUS DEFERENS.
CC -1- SUBCELLULAR LOCATION: STORED IN SECRETORY GRANULES OF GRANULAR
CC CONVOLUTED TUBULES CELLS.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN SUBMANDIBULAR GLAND.
CC -1- DEVELOPMENTAL STAGE: EXPONENTIAL INCREASE BETWEEN DAYS 25 AND 30
CC AFTER BIRTH.
CC -1- INDUCTION: By androgens.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSCRS AG3/AGS; FUNGI SC7/SC14 AND PLANTS PR-1.
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CC
DR EMBL: M92650; AAA37166.1; -
DR EMBL: L05360; AAA37461.1; -
DR PIR: B49202; B49202.
DR MGD: MGI:102552; Aeg2.
DR InterPro: IPR001283; Allrgn_V5/TPX1.
DR Ptm: PF00188; SCP_1.
DR PRINTS: PK00837; VTPXLIKE.
DR ProDom: PD000542; Allrgn_V5/TPX1; 1.

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DR SMART; SM00198; SCP; 1.  
 DR PROSITE; PS01009; SCP\_AGS\_PRL\_SC7\_1; 1.  
 DR PROSITE; PS01010; SCP\_AGS\_PRL\_SC7\_2; 1.  
 DR Sperm; Glycoprotein; Signal.  
 FT SGNAL 1 19  
 FT CHAIN 20 241  
 FT CARBOHYD 118 118 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CARBOHYD 132 132 N-LINKED (GLCNAC... ) (POTENTIAL).  
 FT CARBOHYD 175 175 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 241 AA; 27314 MW; D903788BAE4001BF CRC64;  
 Query Match 10.1%; Score 101; DB 1; Length 241;  
 Best Local Similarity 23.3%; Pred. No. 0.049;  
 Matches 45; Conservative 31; Mismatches 67; Indels 50; Gaps 12;  
 QY 11 ERLDDHREMTTEL--HNGYRAFAFARYKSKRMETVYDCTLEKAKYSAKCEPSS 67  
 DB 29 ERLSTSKSKSYOEELVSKHQLRKYS--GSDLLNENRYDAQVNAQGRDKCTFSPHS 86  
 QY 68 EE-----ENVDFSAATINIPLEAGNSWSEIF-----ELGKRYNNKNGTSHIA- 112  
 DB 87 IELRTNLRKGEN--LFSSTYL-VF-----SSVYQGYTESKGLIFGV-GPKQWASY 135  
 QY 113 -----NMVDSHDKCAVYDCSG---KTHVCCGYEPAKGGK-----TTFEGAPCS 158  
 DB 136 VQHTHYVYKSNLQVACGVAECPEPNLRYFYVCNCPVLTNGHYPSRYLATYARAPCA 195  
 QY 159 RGSYGGAGVYCD 171  
 DB 196 SCPD-----RCED 203  
 RESULT 25  
 ID VAS\_DOLAR STANDARD; PRT; 203 AA.  
 AC 005108;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DE 16-OCT-2001 (Rel. 40, Last annotation update)  
 OS Venom allergen 5 (Antigen 5) (AG5) (Allergen Dol a 5) (Dol a V).  
 OC Dolichovespula aremaria (Yellow hornet).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Endopterygota; Apocrita;  
 OC Aculeata; Vespoidea; Vespidae; Vespinae; Dolichovespula.  
 ON NCBI\_TaxID=7442;  
 RN 11  
 RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=93203603; PubMed=8454859;  
 RA Lu G., Villalba M., Coscia M.R., Hoffman D.R., King T.P.;  
 RT Sequence analysis and antigenic cross-reactivity of a venom  
 RT allergen, antigen 5, from hornets, wasps, and yellow jackets.\*;  
 RL J. Immunol. 150:2823-2830(1993).  
 CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;  
 CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.  
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 CC  
 CC EMBL; M98859; AAA28303.1;  
 DR HSSP; P04284; ICPE.  
 DR InterPro; IPR001283; ALLrgn\_V5/TPX1.  
 DR Pfam; PF00188; SCP; 1.  
 DR PRINTS; PRO0837; V5TPXLIKE.  
 DR PRODOM; PD000542; ALLrgn\_V5/TPX1; 1.  
 DR SMART; SM00198; SCP; 1.  
 DR PROSITE; PS01009; SCP\_AGS\_PRL\_SC7\_1; 1.  
 DR PROSITE; PS01010; SCP\_AGS\_PRL\_SC7\_2; 1.

KM Venom; Allergen.  
 FT DISULFID 4 15  
 FT DISULFID 7 100  
 FT DISULFID 25 93  
 FT DISULFID 169 186  
 SQ SEQUENCE 203 AA; 23202 MW; 6D5C725AD4EBC4B CRC64;  
 Query Match 10.1%; Score 100.5; DB 1; Length 203;  
 Best Local Similarity 19.2%; Pred. No. 0.044;  
 Matches 37; Conservative 31; Mismatches 84; Indels 41; Gaps 6;  
 QY 1 EGYSLICQRETL-----DDMEPTELEHNGYRAFAFARYKT----- 38  
 DB 9 KGHITLCKGTSMKNGCGKLYSYGVTDKNEYLYKHNEFRQVAGGLETRGNPQP 68  
 QY 39 --SKARTVYDCTLEKAKYSAKCEPSSSEBNDVFSATLNIPLGNS----- 89  
 DB 69 PAKNNMLVWDELAKTIQVWANCNGHDQCRNTAKYPGQNVALASTGNSYQTMSTYL 128  
 QY 90 ---WSEIFEL--RGKYNNKNGTSHIANMYDSHDKLCA--VYDCSGKTH-VGQY 139  
 DB 129 IKMEDEVKDYNPVPHDLMHNNFSVGHYQVWVGKTEIGGSVYKTEINKMHTHYLVONY 188  
 QY 140 GPEAKGDKTYE 152  
 DB 189 GPAGNTYMQPYE 201  
 RESULT 26  
 ID PRLA\_LYCES STANDARD; PRT; 175 AA.  
 AC 008697;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DE 15-JUN-2002 (Rel. 41, Last annotation update)  
 OS Pathogenesis-related protein 1A1 precursor (PR-1A1).  
 OS Lycopersicon esculentum (Tomato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Asteridiales; Magnoliophyta; eudicotyledons; core eudicot;  
 OC Asterales; euasterids I; Solanales; Solanaceae; Solanum.  
 ON NCBI\_TaxID=4081;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Rutgers; TISSUE=leaf;  
 RX MEDLINE=94247356; PubMed=8190070;  
 RA Torniero P., Conejero V., Vera P.;  
 RT Tomato is induced upon viral infection of the PR-1 protein family from  
 RT tomato is induced upon viral infection.  
 RL Mol. Gen. Genet. 243:47-53(1994).  
 CC -1- FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF PLANTS  
 CC AGAINST PATHOGENS (BY SIMILARITY).  
 CC -1- INDUCTION: SYNTHESIZED DURING PATHOGEN INFECTION OR OTHER STRESS-  
 CC RELATED RESPONSES.  
 CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;  
 CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.  
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 CC  
 CC EMBL; X71592; CA50596.1;  
 DR HSSP; P04284; ICPE.  
 DR InterPro; IPR001283; ALLrgn\_V5/TPX1.  
 DR Pfam; PF00188; SCP; 1.  
 DR PRINTS; PRO0837; V5TPXLIKE.  
 DR PRODOM; PD000542; ALLrgn\_V5/TPX1; 1.  
 DR SMART; SM00198; SCP; 1.  
 DR PROSITE; PS01009; SCP\_AGS\_PRL\_SC7\_1; 1.  
 DR PROSITE; PS01010; SCP\_AGS\_PRL\_SC7\_2; 1.

KW Plant defense, Pathogenesis-related protein; Signal; Multigene family.  
 FT SIGNAL 1 21 POTENTIAL.  
 FT CHAIN 22 175 PATHOGENESIS-RELATED PROTEIN 1A1.  
 FT DISULFID 65 135 BY SIMILARITY.  
 FT DISULFID 108 114 BY SIMILARITY.  
 FT DISULFID 130 144 BY SIMILARITY.  
 SQ SEQUENCE 175 AA; 19660 MW; 0DF68E89062FAC1 CRC64;  
 Query Match 9.6%; Score 96; DB 1; Length 175;  
 Best Local Similarity 26.4%; Pred. No. 0.093;  
 Matches 39; Conservative 13; Mismatches 48; Indels 48; Gaps 8;  
 OY 18 REMETELHNGYR-----AFAFARYKTSKRTVYDCTLEKAYSAKRC-- 61  
 DB 25 REMFLNHAARRRGVGPMTPDGLAAYVONY-----ANORADDCGM 67  
 OY 62 --SEEPSSEENVDFSAATLNIPLKNGSNMSEIFELRGKRYNKN---GKT-SNINAM 114  
 DB 68 IHSDCPYGEN-----LAAAFPOLNAGAVAMMD--EKQWYDYSNTCAKGVCHYQV 120  
 OY 115 VMDSHDKLCAVYDC-SGKTHVCGGCP 141  
 DB 121 VMKRSVRLCGARVRCNSGWITCNDP 148  
 RESULT 27  
 VA3\_SOLIN STANDARD; PRT; 234 AA.  
 AC P35778; O16135; O8TW22;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Venom allergen III precursor (Allergen Sol r 3) (Sol r III).  
 OS Solenopsis invicta (Red imported fire ant).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Endopterygota; Apocrita;  
 OC Aculeata; Formicidae; Myrmicinae; Solenopsis.  
 NC NCBI\_TaxID=13686;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Venom;  
 RA Hoffman D.R.; Farrar D.; Schmidt M.; McConnell T.J.;  
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.  
 RP SEQUENCE OF 23-234 FROM N.A.  
 RA MEDLINE=96051059; PubMed=8588684;  
 RA Hoffman D.R.;  
 RT Allergy 50:535-544(1995).  
 RL 13  
 RP SEQUENCE OF 23-234.  
 RC TISSUE-Venom;  
 RA Hoffman D.R.; PubMed=8423273;  
 RA Hoffman D.R.;  
 RT Allergens in Hymenoptera venom XXIV: the amino acid sequences of  
 RT imported fire ant venom allergens Sol I II, Sol I III, and Sol I  
 RT IV.";  
 RL J. Allergy Clin. Immunol. 91:71-78(1993).  
 RP PARTIAL SEQUENCE OF 23-45.  
 RC TISSUE-Venom;  
 RA MEDLINE=90285439; PubMed=2355158;  
 RA Hoffman D.R.; Smith A.M.; Schmidt M.; Moffitt J.E.; Guralnick M.;  
 RT Allergens in Hymenoptera venom XXII: Comparison of venoms from two  
 RT species of imported fire ants, Solenopsis invicta and richteri.";  
 RL J. Allergy Clin. Immunol. 85:988-996(1990).  
 CC -1- DISEASE: THE MOST COMMON CAUSE OF INSECT VENOM ALLERGY IN THE  
 CC SOUTHEASTERN UNITED STATES IS THE IMPORTED FIRE ANT.  
 CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;  
 CC INSECTS AG1/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.  
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 CC -----  
 CC EMBL, AF012919; AAB65434.1; -  
 DR PIR; B37330; B37330.  
 DR PIR; C44582; C44582.  
 DR HSP; P04284; ICPE.  
 DR InterPro; IPR001283; Allrgn\_V5/TPx1.  
 DR Pfam; PF00188; SCP; 1.  
 DR PRINTS; PR00837; V5TPXLIKE.  
 DR ProDom; PD000542; Allrgn\_V5/TPx1; 1.  
 DR SMART; SM00198; SCP; 1.  
 DR PROSITE; PS01009; SCP\_AG5\_PRL\_SCT\_1; 1.  
 DR PROSITE; PS01010; SCP\_AG5\_PRL\_SCT\_2; 1.  
 KW Venom; Allergen; Signal.  
 FT SIGNAL 1 22  
 FT CHAIN 23 234 VENOM ALLERGEN III.  
 FT DISULFID 26 41 BY SIMILARITY.  
 FT DISULFID 31 125 BY SIMILARITY.  
 FT DISULFID 52 118 BY SIMILARITY.  
 FT DISULFID 198 216 BY SIMILARITY.  
 FT DISULFID 183 183 G->E (IN REF. 3).  
 FT COMPLECT 194 194 T->S (IN REF. 3).  
 FT COMPLECT 199 199 G->A (IN REF. 3).  
 SQ SEQUENCE 234 AA; 26351 MW; 539F510B59941D83 CRC64;  
 Query Match 9.6%; Score 96; DB 1; Length 234;  
 Best Local Similarity 24.0%; Pred. No. 0.13;  
 Matches 41; Conservative 23; Mismatches 73; Indels 34; Gaps 6;  
 OY 15 DDMREMETELHNGRAAFARNTK-----TSKRTVYDCTLEKAYSAKRCSE 64  
 DB 62 DAEKALYKNNELRQVAVSGKMGNGTPOPPAKPAPNLTWDELATIAORWANOCTFE 121  
 OY 65 PSSEENVDFVS-----AAT-----LNIPLEAGNSWSEIFELRGKRYNKNKTSNI-- 111  
 DB 122 HDA-CRNERFAVGQNTATSSGKKNSTPHEMLLTWYNVADFNRMISFSPSDHILM 180  
 OY 112 ----ANNVMDSHDKLCAV-----DCSGTHVCOYGPAGKDGKTYE 152  
 DB 181 KVGHYTOIVMAKTKIKGCRIMKEPDMMTKHYLVCMYGPAGNVLAGAPIYE 231  
 RESULT 28  
 VA3\_SOLIN STANDARD; PRT; 211 AA.  
 AC P35779;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Venom allergen III (Allergen Sol r 3) (Sol r III).  
 OS Solenopsis richteri (Black imported fire ant).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;  
 OC Aculeata; Formicidae; Myrmicinae; Solenopsis.  
 NC NCBI\_TaxID=30203;  
 RN 11  
 RP SEQUENCE.  
 RC MEDLINE=98049167; PubMed=9389299;  
 RA Hoffman D.R.;  
 RL Reactions to less common species of fire ants.";  
 RL J. Allergy Clin. Immunol. 100:679-683(1997).  
 RP SEQUENCE OF 1-20.  
 RA MEDLINE=90285439; PubMed=2355158;  
 RA Hoffman D.R.; Smith A.M.; Schmidt M.; Moffitt J.E.; Guralnick M.;  
 RT Allergens in Hymenoptera venom XXII: Comparison of venoms from two  
 RT species of imported fire ants, Solenopsis invicta and richteri.";  
 RL J. Allergy Clin. Immunol. 85:988-996(1990).  
 CC -1- DISEASE: THE MOST COMMON CAUSE OF INSECT VENOM ALLERGY IN THE

CC SOUTHEASTERN UNITED STATES IS THE IMPORTED FIRE ANT.  
 CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;  
 CC INSECTS AG3/AG5; FUNGI SCT/SCI4 AND PLANTS PR-1.  
 DR PIR: D60727; D60727.  
 DR HSP: P04284; ICPE.  
 DR InterPro: IPR001283; Allrgn\_V5/TPx1.  
 DR Pfam: PF00188; SCP; 1.  
 DR PRINTS: PR00837; V5TPX1KE.  
 DR PRODOM: PD000542; Allrgn\_V5/TPx1; 1.  
 DR SMART: SM00198; SCP; 1.  
 DR PROSITE: PS01009; SCP\_AGS\_PRL\_SCT\_1; 1.  
 DR PROSITE: PS01010; SCP\_AGS\_PRL\_SCT\_2; 1.  
 DR Venom: Allergen.  
 SQ SEQUENCE 211 AA; 23869 MW; 99683BBA72844E9B CRC64;  
 Query Match 9.6%; Score 95.5; DB 1; Length 211;  
 Best Local Similarity 21.5%; Pred. No. 0.13; Mismatches 6;  
 Matches 38; Conservative 21; Indels 47; Gaps 6;  
 OY 15 DDHMEFTELHNGYRAAFAANK-----TSKRTMYD-----CTLE 51  
 DB 40 DAEDDAVKNHNLKQRYASGKEMKNGPQPAVAMPULWDEPLATIAQRANOCCTE 99  
 OY 52 EKAKSKSEKS-----EPPSEENVDVFSATLNIPLDAGNSWSEIFELRGKYNNKG 106  
 DB 100 HDRCANRYERAVGONIAATSSGKNKSTLSDML-----LWYNEKDFDRWISSP 151  
 OY 107 KTSNI-----ANNVMSHDKLCQAVY-----DCSGRTYVCOYCPGKSGDKTYIE 152  
 DB 152 SDGNILMHVGHVQTQVIMAKTKIGCRIMFKEDNNKHYLVNCGPAGNVLAGQIYE 208  
 RESULT 29  
 VAS\_POLFU STANDARD; PRT; 205 AA.  
 ID VAS\_POLFU  
 AC P35780;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE Venom allergen 5 (Antigen 5) (AG5) (Allergen pol f 5) (pol f V).  
 OS Polistes fuscatus (Paper wasp).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;  
 OC Aculeata; Vespoidea; Vespidae; Polistinae; Polistes.  
 OX NCBI\_TaxID=30207;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE-Venom.  
 RX MEDLINE=94044316; PubMed=8227862;  
 RA Hoffman D.R.;  
 RT Allergens in Hymenoptera venom. XXV: The amino acid sequences of  
 RT antigen 5 molecules and the structural basis of antigenic cross-  
 RT reactivity.\*;  
 RL J. Allergy Clin. Immunol. 92:707-716(1993).  
 CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;  
 CC INSECTS AG3/AG5; FUNGI SCT/SCI4 AND PLANTS PR-1.  
 DR PIR: E44523; E44522.  
 DR PIR: E44523; E44522.  
 DR HSP: P04284; ICPE.  
 DR InterPro: IPR001283; Allrgn\_V5/TPx1.  
 DR Pfam: PF00188; SCP; 1.  
 DR PRINTS: PR00837; V5TPX1KE.  
 DR PRODOM: PD000542; Allrgn\_V5/TPx1; 1.  
 DR SMART: SM00198; SCP; 1.  
 DR PROSITE: PS01009; SCP\_AGS\_PRL\_SCT\_1; 1.  
 DR PROSITE: PS01010; SCP\_AGS\_PRL\_SCT\_2; 1.  
 DR Venom: Allergen.  
 FT DISULEID 4 16 BY SIMILARITY.  
 FT DISULEID 8 104 BY SIMILARITY.  
 FT DISULEID 28 96 BY SIMILARITY.  
 FT DISULEID 171 188 BY SIMILARITY.  
 SQ SEQUENCE 205 AA; 23068 MW; 77308250FBF2357 CRC64;

Query Match 9.5%; Score 95; DB 1; Length 205;  
 Best Local Similarity 18.9%; Pred. No. 0.14;  
 Matches 37; Conservative 30; Mismatches 79; Indels 50; Gaps 7;  
 OY 2 GDYSICQGRK-----DDDKREFTLHNGYRAAFAANKYK----- 38  
 DB 11 GHTVCOYESTKPSKCNADKVIKSGPTEERKLTIVENHRRQKVAQGLTRGNGPQ 70  
 OY 39 ---SKRTVYCTLEEKAKSKAKSEEPSEENVDVFSATLNIPLDAGNS----- 89  
 DB 71 PAASDNNILVMDLHIAQVMAQQQLLVHDKCRNTAKTQVQ-NIAVAGSKLPDVS 129  
 OY 90 ---WSEIFELRGKYNNK-----GKTSNIANNVMSHDKLCQAVYDCSRT----HV 135  
 DB 130 LRLWNEVQDN---NKGITRQNGKGVHTQVIMAKTKIGCSLKYNNKNNQHLYL 186  
 OY 136 VCOYCPGKSGDKTYIE 151  
 DB 187 ICNYPGAGNYLGOLPY 202  
 RESULT 30  
 YJH9\_YEAST STANDARD; PRT; 299 AA.  
 ID YJH9\_YEAST  
 AC P47032;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical 30.6 kDa protein in SCP160-SMC3 intergenic region  
 DE precursor.  
 DE YJ079C OR J1022.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=5288;  
 RX MEDLINE=26093911; PubMed=7483841;  
 RA Mosega T., Schaffli-Gerstenschlaeger I., Chalwatzi N., Baur A.,  
 RA Botes E., Fournier C., Schmitt S., Veltin C., Wilhelm N.,  
 RA Zimmermann F.K.;  
 RT Sequence analysis of a 33.1 kb fragment from the left arm of  
 RT Saccharomyces cerevisiae chromosome X, including putative proteins  
 RT with leucine zippers, a fungal Zn(II)-Cys6 binuclear cluster domain  
 RT and a putative alpha 2-SCB-alpha 2 binding site.\*;  
 RL Yeast 11:681-689(1995).  
 CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;  
 CC INSECTS AG3/AG5; FUNGI SCT/SCI4 AND PLANTS PR-1.  
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 CC EMBL: 249354; CAA89372.1;  
 DR EMBL: X83502; CAA58491.1;  
 DR EMBL: X88851; CAA61315.1;  
 DR HSP: P04284; ICPE.  
 DR SGD: S0003615; YJL079C.  
 DR InterPro: IPR001283; Allrgn\_V5/TPx1.  
 DR Pfam: PF00188; SCP; 1.  
 DR PRODOM: PD000542; Allrgn\_V5/TPx1KE.  
 DR PRINTS: PR00837; V5TPX1KE.  
 DR SMART: SM00198; SCP; 1.  
 DR PROSITE: PS01009; SCP\_AGS\_PRL\_SCT\_1; 1.  
 DR PROSITE: PS01010; SCP\_AGS\_PRL\_SCT\_2; 1.  
 DR Hypothetical protein; Signal.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 299 HYPOTHEETICAL PROTEIN YJL079C.

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FT DOMAIN 102 165 ALA/SER/THR-RICH.
SQ SEQUENCE 299 AA; 30634 MW; A116769CA87C5679 CRC64;
Query Match 9.5%; Score 95; DB 1; Length 299;
Best Local Similarity 22.0%; Pred. No. 0.22;
Matches 36; Conservative 27; Mismatches 43; Indels 58; Gaps 10;
QY 14 DDDREFFTEL---HNGYR-----AAFAANYTSMKRTMYDC--TLEEK 53
DB 156 DSDLSDBASVLAENKRAALHKDTPALMSDPLASIDYADN-----TDCGILTH- 208
QY 54 AKKAEKCESEPESEENVDVFSATLNIPL-----EAGNSWSEI--FELRGKVTNKG 106
DB 209 -----SCGPYGE-----NLALGTDGPALADVANYENISYDPSNPGFSN- 247
QY 107 KTSNANWVDSHDKLCAVYDCSGK--THVCGQYCPKAGDK 148
DB 248 -TGHFTGVYMKSTYGVCGIKTCGAGNDYVTCSTYDPAGNYGE 290

RESULT 31
PR1_SAMNI STANDARD; PRT; 167 AA.
ID PR1_SAMNI
AC 041359;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pathogenesis-related protein PR-1 type precursor.
OS Sambucus nigra (European elder).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Dipscales; Adoxaceae; Sambucus.
OX NCBI_Taxid:4202;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-abscission zone;
RA Coupe S.A., Taylor J.E., Roberts J.A.;
RT Submitted (DEC1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF PLANTS
CC -1- AGAINST PATHOGENS.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SCT/SC14 AND PLANTS PR-1.
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CC
CC EMBL; 246947; CAAB7071.1;
CC HSSP; P04284; ICFE.
CC InterPro; IPR001283; Allrgn_V5/Tpx1.
CC Pfam; PF00188; SCP.1.
CC PRINTS; PR00837; VSTPLKE.
CC PRODOM; PD000542; Allrgn_V5/Tpx1.1.
CC SMART; SM00198; SCP.1.
CC PROSITE; PS01009; SCP_AGS_PRL_SCT_1; 1.
CC PROSITE; PS01010; SCP_AGS_PRL_SCT_2; 1.
CC K1 plant defense; Pathogenesis-related protein; Signal.
CC SIGNAL 1 25
CC CHAIN 30 167 PATHOGENESIS-RELATED PROTEIN PR-1 TYPE.
CC FT DISULFID 72 144 BY SIMILARITY.
CC FT DISULFID 117 123 BY SIMILARITY.
CC FT DISULFID 139 153 BY SIMILARITY.
CC SEQUENCE 167 AA; 18410 MW; 4F2BMB3269392E53 CRC64;
SQ
Query Match 9.5%; Score 94.5; DB 1; Length 167;
Best Local Similarity 23.2%; Pred. No. 0.12;
Matches 42; Conservative 18; Mismatches 50; Indels 71; Gaps 9;
QY 4 YSLCQOREKLDMDREMTTELHNGYR-----AAFAANYTSMKRTMYDC 49

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DB 25 IYSAQ-----NSPGQYVDANHAARSANVNGPYTWDESVAAAFYAGSR-----AGCR 73
QY 50 LEEAKAKSEKSEPESEENVDVFSATLNIPLLEAGNSWSEIELGK-----100
DB 74 LVH-----SDPFRGE-----NLARGSG-----FELGRNANVMVAE 106
QY 101 --VYNNNGKT-----SNANWVDSHDKLCAVYDC--SGKHVYCGQCPKAGDKTI 150
DB 107 RNDINNTNITCAKPGKVGCHTGYVMMKNSVRIICANVCANRCNMAFICNTSPRGNTAGQRP 166
QY 151 Y 151
DB 167 Y 167

RESULT 32
CRSL_HUMAN STANDARD; PRT; 249 AA.
ID CRSL_HUMAN
AC P54107; Q13248; C00698; Q14082;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cysteine-rich secretory protein-1 precursor (acidic epididymal
DE glycoprotein homolog) (AEG-1-like protein) (ARP).
GN AEG1 OR CRISP-1.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid:9606;
RN [1]
RP SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS), AND SEQUENCE OF 22-41.
RX MEDLINE-96270732; PubMed-8665901.
RA Kraetschmar J., Haendler B., Eberspaecher U., Roostermann D.,
RA Donner P., Schlenker W.-D.;
RT "The human cysteine-rich secretory protein (CRISP) family. Primary
RT structure and tissue distribution of CRISP-1, CRISP-2 and CRISP-3."
RL Eur. J. Biochem. 236:827-836(1996).
RN [2]
RP SEQUENCE FROM N.A. (LONG ISOFORM).
RX MEDLINE-96103955; PubMed-8543280.
RA Hayashi M.;
RT "Analysis of the human acidic epididymal glycoprotein-like molecule:
RT isolation of cDNA and tissue localization."
RL Hokkaido Igaku Zasshi 70:743-753(1995).
RN [3]
RP SEQUENCE FROM N.A. (LONG ISOFORM), AND CHARACTERIZATION.
RX MEDLINE-96435914; PubMed-8838800.
RA Hayashi M., Fujimoto S., Takano H., Uehiki T., Abe K., Ishikura H.,
RA Hayashi M.C., Kirchhoff C., Ishibashi T., Kasahara M.;
RT "Characterization of a human glycoprotein with a potential role in
RT sperm-egg fusion: cDNA cloning, immunohistochemical localization,
RT and chromosomal assignment of the gene (AEG1)."
RL Genomics 32:367-374(1996).
CC -1- FUNCTION: MAY HAVE A ROLE IN SPERM-EGG FUSION AND MATURATION.
CC -1- SUBCELLULAR LOCATION: LOCATED IN THE LUMEN AND EPITHELIUM OF
CC DISTAL DUCTUS EPIDIDYMUS AND EPIDIDYMAL DUCTS. AND ON THE
CC POSTACROSOMAL REGION OF THE SPERM HEAD.
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; a long form (shown here) and a
CC short form/CRISP-1 delta; may be produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: CAPUT CORPUS AND CAUDA REGIONS OF THE
CC EPIDIDYMUS. THE DUCTUS DEFERENS, SPERM AND SEMINAL PLASMA.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCT/TPX1;
CC INSECTS AG3/AG5; FUNGI SCT/SC14 AND PLANTS PR-1.
CC
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DR EMBL: X95237.1: CA64523.1: -
DR EMBL: X95238.1: CA64523.1: -
DR EMBL: S80310.1: AAB35893.1: -
DR EMBL: D38451.1: BAA07483.1: -
DR GenBank: HGNC:304: ABGL.
DR MIM: 601193: -
DR InterPro: IPR001283: Allrgn_V5/Tpx1.
DR Pfam: PF00188: SCP_1.
DR PRINTS: PRO0837: V5TPXLKE.
DR ProDom: PD000542: Allrgn_V5/Tpx1.1.
DR SMART: SM00198: SCP_1.
DR PROSITE: PS01009: SCP_AGS_PRI_SCP_1; 1.
DR PROSITE: PS01010: SCP_AGS_PRI_SCP_2; 1.
DR GlycoProtein: Signal; Multigene family; Alternative splicing.
KW SIGNAL.
FT CHAIN 1 21
FT CARBOHYD 22 249 Cysteine-rich secretory protein-1.
FT VARSPLIC 178 178 E->D (IN SHORT ISOFORM).
FT VARSPLIC 179 249 MISSING (IN SHORT ISOFORM).
FT CONFLICT 22 22 K->E (IN REF. 2 AND 3).
FT CONFLICT 97 97 T->A (IN REF. 2 AND 3).
SQ SEQUENCE 249 AA: 28481 MW: 85BED3DEAD62A9C CRC64;

Query Match
Best Local Similarity 9.5%; Score 94.5; DB 1; Length 249;
Matches 51; Conservative 22; Mismatches 67; Indels 75; Gaps 14;

OY 9 GREKIDDM---REMFELHNGYRAAFARNTKSKRMVYDCTLEKAYKSAKSEEP 65
DB 29 QFNKLVTDLPNVEELVNIHNLRRVVP--PASNMLKMSW-----SEEA 71
OY 66 SSEEENVDFSA---ATINIPLE-----AGNSW-----SEIFELRGKVVY--- 103
DB 72 A---QNAIFSKYCMETESNPLERLPNFCEGNHMTSPYMSVIT---GVWYSEST 125
OY 104 -KNGK-----TSNANWVMSHDKLGCAVYCC---SGKHVYCOY---GPEAK 144
DB 126 FKNGEWTDDDDITTDHYTQVWATSTYLIGCALASCRGGSPRLVYCHCHGNDPEK 185
OY 145 GDDGTIEBAGARCSCSDYAGVYCDODDQNLICI 179
DB 186 NEP---YKTVGPCACPS-----NCEBKICITNPICI 212

RESULT 33
SC7_SCHCO STANDARD; PRT; 204 AA.
AC P35794.1
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Fruiting body protein SC7 precursor.
GN SC7
OS Schizophyllum commune (Bracket fungus).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Agaricales; Schizophyllaceae; Schizophyllum.
OX NCBI_Taxid=5334;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94065639; PubMed=8245835;
RA Schuren F.H.J., Asgeltsdottir S.A., Kothe E.M., Scheer J.M.J.,
RA Wessels J.G.H.;
RT "The Sc7/Sc14 gene family of schizophyllum commune codes for
RT extracellular proteins specifically expressed during fruit-body
RT formation."
RL J. Gen. Microbiol. 139:2083-2090(1993).
CC -1- SUBCELLULAR LOCATION: secreted.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED ONLY IN FRUITING DIKARYONS.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1,
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
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CC -----
DR EMBL: M81722.1: AAA16207.1: -
DR PIR: S27448; S27448.
DR HSP: P04284; ICEF.
DR InterPro: IPR001283: Allrgn_V5/Tpx1.
DR Pfam: PF00188: SCP_1.
DR PRINTS: PRO0837: V5TPXLKE.
DR ProDom: PD000542: Allrgn_V5/Tpx1.1.
DR SMART: SM00198: SCP_1.
DR PROSITE: PS01009: SCP_AGS_PRI_SCP_1; 1.
DR PROSITE: PS01010: SCP_AGS_PRI_SCP_2; 1.
DR Fruiting body; Signal; Multigene family.
KW SIGNAL.
FT CHAIN 1 16
FT CARBOHYD 17 204 FRUITING BODY PROTEIN SC7.
FT CARBOHYD 118 118 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 204 AA: 22302 MW: 47FIC845ADPA2FC9 CRC64;

Query Match
Best Local Similarity 9.4%; Score 94; DB 1; Length 204;
Matches 35; Conservative 23; Mismatches 62; Indels 42; Gaps 5;

OY 10 REKIDDMR-----EMFELHNGYRAAFARNTKSKRMVYDCTLEK 53
DB 34 RSPIDIDRSADALANAPPOSEIDWIKAHNNRONG-----AAVWMDLSDK 86
OY 54 AKSAKSEEPSESEENVDFSAATINIPLE-----EAGNSWSTIFELRKRYNNKGTSN 110
DB 87 ADPAVASCITWHSNCGNLAWFSPQAKFKMTISGVGCHNALEPPIYNTTYSAGHWIQ 146
OY 111 IANWVMSHDKLGCAVYDCSKT-----HYVCOY 139
DB 147 V---VWKSITVSGCAVSCPGLGKRPDPKTKLWYVCNY 185

RESULT 34
AGC_RAT STANDARD; PRT; 246 AA.
AC P12020.
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sperm-coating glycoprotein precursor (SCP) (acidic epididymal
DE glycoprotein) (Protein D) (Protein E) (Staloprotein)
DE (32 kDa epididymal protein).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Epидidymis; PubMed=3780731;
RX MEDLINE=87053995; PubMed=87053995;
RA Brooks D.E., Means A.R., Wright E.J., Singh S.P., Tiver K.K.;
RA "Molecular cloning of the cDNA for androgen-dependent sperm-coating
RT glycoproteins secreted by the rat epididymis."
RL Eur. J. Biochem. 161:13-18(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89039913; PubMed=2460753;
RA Charest N.J., Joseph D.R., Wilson E.M., French F.S.;
RA "Molecular cloning of complementary deoxyribonucleic acid for an
RT androgen-regulated epididymal protein: sequence homology with
RT metalloproteins."
RL Mol. Endocrinol. 2:999-1004(1988).
CC -1- FUNCTION: THIS PROTEIN IS SUPPOSED TO HELP SPERMATOZOA UNDERGO
CC FUNCTIONAL MATURATION WHILE THEY MOVE FROM THE TESTIS TO THE

```

CC DUCTUS DEFERENS.  
CC -1- INDUCTION: BY ANDROGENS.  
CC MISCELLANEOUS: SCP IS AN ANDROGEN-DEPENDENT PROTEIN, WHICH IS  
CC SECRETED BY THE EPIDIDYMAL EPITHELIUM AND THEN BECOMES ASSOCIATED  
CC WITH THE SPERM SURFACE. TWO MAJOR VARIANT PROTEIN D AND E DIFFER  
CC FROM EACH OTHER BY THEIR CARBOHYDRATE SIDE CHAINS.  
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;  
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.  
CC  
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CC  
CC EMBL: X04643; CAA28304.1; -  
CC EMBL: M31173; AAB59716.1; -  
CC PIR: A40918; A40918.  
CC InterPro: IPR001283; Allrgn\_V5/7px1.  
CC Pfam: PF00188; SCP.1.  
CC PRINTS: PR00837; V5TPXLIKE.  
CC ProDom: PD000542; Allrgn\_V5/7px1.1.  
CC SMART: SM00198; SCP.1.  
CC PROSITE: PS01009; SCP\_AG5\_PRL\_SC7\_1; 1.  
CC PROSITE: PS01010; SCP\_AG5\_PRL\_SC7\_2; 1.  
CC KW Sperm; Glycoprotein; Signal.  
CC SIGNAL 1 19  
CC CHAIN 1 20  
CC MOD\_RES 20 20  
CC CARBOHYD 32 32  
CC CARBOHYD 85 85  
CC CARBOHYD 147 147  
CC CARBOHYD 213 213  
CC SEQUENCE 246 AA; 27847 MW; 585207C7CF7CE9D CRC64;  
SQ  
Query Match 9.4%; Score 94; DB 1; Length 246;  
Best Local Similarity 23.2%; Pred. No. 0.21; Index 44; Gaps 9;  
Matches 45; Conservative 23; Mismatches 82;  
DB 17 MRBMTLEHNGYRAAPRNKTKMTMYDCTLEEKAYSAKCESEPSSEENV--- 72  
DB 40 VDEEILNHNDLRNTVSPS--GSDLRVEMBDADAVNNAQMANRCIYNHSPDQHTTTLK 97  
DB 73 --DVFSAATINPLEAGN---SWNSEIFE-LRGKRYNKG-KTSNIAMVWDSHDKLC 124  
DB 98 CGENLEFMA--NYPASMSVYIDWDYDSDLEDFGFGPKYGVGHYGTQVWNSSTFLVAC 154  
DB 125 AAVDSCG--KTHVVCQYGFPEANGDK--TIYEGAPC----- 157  
DB 155 GVAECDDPPLKFFYVCHYCPGNGYVGRILSPYTBEGPCDSCPGNCBDGLCTNSCEYEDNY 214  
DB 158 SRCSDYGAGVTCD 171  
DB 215 SNGCDLKKVSCDD 228  
RESULT 35  
PRL3\_HORVU STANDARD; PRT; 164 AA.  
AC P35792;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Pathogenesis-related protein PRB1-2 precursor.  
OS Hordeum vulgare (Barley).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Triticeae; Hordeum.  
OX NCBI\_Taxid=4513;  
RN [1]

RE SEQUENCE FROM N.A.  
RC STRAIN-CV. PEAKNON RESISTANT; TISSUE-Leaf;  
RX MEDLINE=95036024; PubMed=7524728;  
RA Moudrov A., Moudrova E., Scott K.J.;  
RT "Gene family encoding basic pathogenesis-related 1 proteins in  
barley.";  
RL Plant Mol. Biol. 26:503-507(1994).  
CC -1- FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF PLANTS  
CC AGAINST PATHOGENS.  
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;  
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.  
CC  
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CC  
CC EMBL: Z26320; CAA81229.1; -  
CC PIR: S37188; S37188.  
CC HSP: P04284; ICPE.  
CC InterPro: IPR001283; Allrgn\_V5/7px1.  
CC Pfam: PF00188; SCP.1.  
CC PRINTS: PR00837; V5TPXLIKE.  
CC ProDom: PD000542; Allrgn\_V5/7px1.1.  
CC SMART: SM00198; SCP.1.  
CC PROSITE: PS01009; SCP\_AG5\_PRL\_SC7\_1; 1.  
CC PROSITE: PS01010; SCP\_AG5\_PRL\_SC7\_2; 1.  
CC KW Plant defense; Pathogenesis-related protein; Signal; Multigene family.  
CC SIGNAL 1 14  
CC CHAIN 1 14  
CC MOD\_RES 25 25  
CC CARBOHYD 144 144  
CC DISULFID 68 140  
CC DISULFID 113 119  
CC DISULFID 135 139  
CC SEQUENCE 164 AA; 17679 MW; DB8722DB/4EB390 CRC64;  
SQ  
Query Match 9.3%; Score 92.5; DB 1; Length 164;  
Best Local Similarity 24.0%; Pred. No. 0.18; Index 43; Gaps 6;  
Matches 36; Conservative 15; Mismatches 56;  
DB 25 HNGYRA-----AFARNYTSKMTMYDCTLEEKAYSAKCESEPSSE 70  
DB 35 HNAARSVGVGAVSWSTKLQAFQNTANQR---INDKLOHSG-----GPYGE 79  
DB 71 NVDFSAATINPLEAGNSWSEIFEELRGKRYNKGK-----SNIAWVWDSHDKLC 123  
DB 80 NIFGSGADMKAAADVNSWNE-----KRDYNGSNTCAAGKYGCHYTOVWNSASTSIG 134  
DB 124 CAVVDCSGK--KTHVVCQYGFPEANGDK--TIYEGAPC----- 151  
DB 135 CARVVCNNRGVETTCNEPRNTYGVGRPY 164  
RESULT 36  
PRL3\_HORVU STANDARD; PRT; 164 AA.  
AC P35793;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Pathogenesis-related protein PRB1-3 precursor (PR-1B) (HV-8).  
OS Hordeum vulgare (Barley).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Triticeae; Hordeum.  
OX NCBI\_Taxid=4513;  
RN [1]  
SEQUENCE FROM N.A.  
RC STRAIN-CV. PEAKNON resistant, and cv. NK1558; TISSUE-Leaf;

```

RA MEDLINE-95036024; PubMed-7524728;
RA Mouradov A., Mouradova E., Scott K.J.;
RT Gene family encoding basic pathogenesis-related 1 proteins in
RT barley.
RL Plant Mol. Biol. 26:503-507(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CV, Palis; TISSUE-Leaf;
RC MEDLINE-94281675; PubMed-8012045;
RA Bryngelsson T., Sommer-Knudsen H.,
RA Ek B., Thordal-Christensen H.;
RT "Purification, characterization, and molecular cloning of basic PR-1-
RT type pathogenesis-related proteins from barley."
RL M1. Plant Microbe Interact. 7:267-275(1994)
CC -1- FUNCTION: PROBABLY INVOLVED IN THE DEEPEN REACTION OF PLANTS
CC AGAINST PATHOGENS.
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC -----
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CC -----
DR EMBL; Z26321; CAAB1230.1;
DR EMBL; Z26333; CAAB1234.1;
DR EMBL; X74940; CAAS2894.1;
DR PIR; S37189; S37189.
DR PIR; S37209; S37209.
DR PIR; S37167; S37167.
DR HSSP; P04284; ICFE.
DR InterPro; IPRO01283; Allrgn_V5/Tpx1.
DR Pfam; PF00188; SCP; 1.
DR PRINTS; PR00837; V5TPX1KE.
DR ProDom; PD000542; Allrgn_V5/Tpx1; 1.
DR SMART; SM00198; SCP; 1.
DR PROSITE; PS01009; SCP_AG5_PRL_SC7_1; 1.
DR PROSITE; PS01010; SCP_AG5_PRL_SC7_2; 1.
KW Plant defense; Pathogenesis-related protein; signal; Multigene family.
FT SIGNAL 1 24
FT CHAIN 25 164 PATHOGENESIS-RELATED PROTEIN PR1-3.
FT MOD_RES 25 25 PYROLIDONE CARBOXYLIC ACID
FT DISULFID 68 140
FT DISULFID 113 119
FT DISULFID 135 150
SQ SEQUENCE 164 AA; 17697 MW; DA4B279B95FC50C6 CRC64;
Query Match
Best Local Similarity 9.3%; Score 92.5; DB 1; Length 164;
Matches 37; Conservative 14; Mismatches 56; Indels 43; Gaps 6;
OY 25 HNGYRA-----AFARNTKTSKMTNRYDCTLEKAYKSAEKSEEPSSEE 70
DB 35 HNAARAAVGVAVSNSTLQAFANQNR-----INDKLOHSG-----GPYGE 79
OY 71 NVDVSAATLNIPLDAGNSWSEIFELRGKYNKNGKT-----SNIANMYWDSHDKLG 123
DB 80 NIFWGSAGADWKASDAVSWYSE-----KKDDYGSNTCAAGKVGHYQYVWRASTSIG 134
OY 124 CAVVDCSGK--THVVCQYGPPEAKDGKTYI 151
DB 135 CARVVCNNRGVFTICNTEPRGNIVGQKPY 164

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DT 15-JUL-1999 (Rel. 38, last sequence update)
DT 15-JUL-1999 (Rel. 38, last annotation update)
DE Venom allergen 5 (Antigen 5) (AG5) (Allergen Vesp m 5).
OS Vespa manducaria (Hornet).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC Aculeata; Vespoidae; Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=446;
RN [1]
RP SEQUENCE.
RC Tissue-Venom;
RC Hoffman D.R., Schmidt J.O.;
RL Submitted (FEB-1998) to the SWISS-PROT data bank.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC -----
CC InterPro; IPRO01283; Allrgn_V5/Tpx1.
CC Pfam; PF00188; SCP; 1.
CC PRINTS; PR00837; V5TPX1KE.
CC ProDom; PD000542; Allrgn_V5/Tpx1; 1.
CC SMART; SM00198; SCP; 1.
CC PROSITE; PS01009; SCP_AG5_PRL_SC7_1; 1.
CC PROSITE; PS01010; SCP_AG5_PRL_SC7_2; 1.
KW Venom; Allergen.
FT DISULFID 4 16
FT DISULFID 8 101
FT DISULFID 26 94
FT DISULFID 168 185
SQ SEQUENCE 202 AA; 22547 MW; 686351357B014EF CRC64;
Query Match
Best Local Similarity 9.3%; Score 92.5; DB 1; Length 202;
Matches 39; Conservative 27; Mismatches 70; Indels 31; Gaps 7;
OY 11 ERDDDMKEMTELEHNGYRAAFARNTK-----SKARTNYDCTLEKAYKSAEK 60
DB 40 EKLE-----ILQHNERKOKVAGLETGKRGPOPPKASNTLVNDELADIAVWAGQ 93
OY 61 C-----SEPSSEEN--DVSATLNIPLDAGNSWSEIFELR-GKYNKNGKTS 109
DB 94 COYGHDCVCRNTRKYSVGNQNAENGSTAFASVSANVQMDADVKNKYOGSTKNLLIEVG 153
OY 110 NIANMYWDSHDKCAVADC--SG--KTHVVCQYGPPEAKDGKTYI 152
DB 154 HYQVWMAKTKIEGSGIKIENGWHRHLYCNGPAGNIGNEPIYE 200

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RESULT 38
PRLA_TOBAC STANDARD; PRT; 168 AA.
AC P08299;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pathogenesis-related protein 1a precursor (PR-1a).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; eusterids I; Solanales; Solanales; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV, Samsun NN;
RC MEDLINE-86015528; PubMed-3658669;
RA Cornelissen B.J.C., Horowitz J., van Kan J.A.L., Goldberg R.B.,
RA Bol J.F.;
RT "Structure of tobacco genes encoding pathogenesis-related proteins
RT from the PR-1 group."
RL Nucleic Acids Res. 15:6799-6811(1987).

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RP SEQUENCE FROM N.A.
RC STRAIN-CV, Samsun NN;
RC MEDLINE-86083593; PubMed-3691804;
RA Onshima M., Matsuoaka M., Yamamoto N., Tanaka Y., Kano-Murakami Y.,

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**Tue Jul 15 09:48:49 2003**

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Page 22

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135 VVOCYGPBANKGDKT1 151
189 YLIONGYPAGNYIGOLPY 206

RESULT 42
ID      TB5_HUMAN
AC      P18084;
DT      01-NOV-1990 (Rel. 16, Created)
DT      01-NOV-1990 (Rel. 16, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Integrin beta-5 precursor.
GN      ITGB5.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX      NCBI_Taxid:9606;
[1]
SEQUENCE FROM N.A.
RC      TISSUE=Thymic epithelium;
RC      MEDLINE=90228356; PubMed=2328726;
RA      Ramaswamy H., Hemler M.E.;
RT      "Cloning, primary structure and properties of a novel human integrin
RL      beta 5 subunit.";
RN      EMBO J. 9:1561-1568(1990).
[2]
SEQUENCE FROM N.A.
RC      MEDLINE=90319111; PubMed=2311275;
RA      Suzuki S., Huang Z.S., Tanikawa H.;
RT      "Cloning of an integrin beta subunit exhibiting high homology with
RL      integrin beta 3 subunit.";
RN      Proc. Natl. Acad. Sci. U.S.A. 87:5354-5358(1990).
[3]
SEQUENCE FROM N.A.
RC      MEDLINE=91009141; PubMed=2211615;
RA      Medendorp J.M., Vestal D.J., Cheresesh D.A., Bodary S.C.;
RT      "cDNA sequence of the human integrin beta 5 subunit.";
RN      J Biol. Chem. 265:17126-17131(1990).
[4]
SEQUENCE FROM N.A.
RC      TISSUE=Kidney;
RA      Strausberg R.;
RL      Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
-1- FUNCTION: INTEGRIN ALPHA-V/BETA-5 IS A RECEPTOR FOR FIBRONECTIN.
IT RECOGNIZES THE SEQUENCE R-G-D IT ITS LIGAND.
-1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. BETA-5
ASSOCIATES WITH ALPHA-V.
-1- SUBCELLULAR LOCATION: Type I membrane protein.
-1- SIMILARITY: BELONGS TO THE INTEGRIN BETA CHAIN FAMILY.
-1- SIMILARITY: CONTAINS 1 VWFA-LIKE DOMAIN.
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-----
CC      EMBL, X53002; CAA37188.1;
CC      EMBL, M35011; AAA52707.1;
CC      EMBL, J05633; AAA59183.1;
CC      EMBL, BC006541; AAH05541.1;
CC      PIR, A35775; A35775.
CC      PIR, S12534; S12534.
CC      PIR, A38308; A38308.
CC      PIR, S11708; S11708.
CC      HSP, P05106; IJY2.
CC      GeneW, HGNC:6160; ITGB5.
CC      MIM: 147561;
CC      InterPro: IPR000561; EGF-like.
CC      InterPro: IPR003369; Integrin_B.

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Query Match	Similarity	Score	db	Length	799:
Best Local	51:	Conservative	31:	Mismatches	66: Indels 84: Gaps 15:
11	EXKDDDMKMPETLHNYRAAFARNKSKSKRTWYD-----	CTLEE-KAYKSAB	59		

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Db      358 EILDGSKRTIQLINNA-----NIRKRVLSVWDDPEDLNLFATCCDGVSYPCOR 411
QY      60 KCSPESESEENVYFSAATLNIPLEA---GSMNSEIFELRGVYNNK---GKTSNIAN 113
Db      412 KC-----EGLNIGTAFSEVLEARSCPRREHEFALRPVGFDSLEGVYNTCT- 462
QY      114 MWDSHDKLGCAV-----VDCSGK-TWV--VCOYGPPE-----AKGPGKTYE----- 152
Db      463 -----CGCSVGLSEPRSAKNGSGTYVCGKCECSPGLATRCCEODDENOSYONLCR 514
QY      153 -----BGAV-----CSNCS-----DYSGVYCDP-----DMONLTCIGH 161
Db      515 EAGNRKLGSGRGDCSCNCCGCFSESGKTYGPFCCDMSFCANRKYVLSGSH 566

RESULT 43
PRLABATH STANDARD: PRT: 161 AA.
AC P33154.
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
GN At2g14610 OR T6B13.15.
OS Arabidopsis thaliana (mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eurosid II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN-CV. Landsberg erecta; TISSUE-Leaf;
RX MEDLINE=93005717; PubMed=1392589;
RA Oknes S., Mauch-Mani B., Moyer M., Potter S., Williams S.,
RA Dincher S., Chandler D., Slusarenko A., Ward E., Ryals J.,
RA "Acquired resistance in Arabidopsis."
RA Plant Cell 4:645-656(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. Columbia;
RX MEDLINE=20083467; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buel C.R., Ketchum K.A., Lee J.J., Renning C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., Pal G., Van Aken S., Umayam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carreira A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Cohenhaver G.P., Preuss D.,
RA Niernsen W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RA "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RA thaliana."
RA Nature 402:761-768(1999).
RT Nature 402:761-768(1999).
RI -1- FUNCTION: PARTIALLY RESPONSIBLE FOR ACQUIRED PATHOGEN RESISTANCE.
RI -1- SUBCELLULAR LOCATION: ACCUMULATES IN THE APOPLAST BEFORE
RI SECRETION.
RI -1- INDUCTION: INDUCED BY 2,6-DICHLOROSANTONIC ACID (TNA) AND
RI SALICYLIC ACID (POSSIBLY AN ENDOGENOUS SIGNAL FOR ACQUIRED
RI RESISTANCE).
RI -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
RI INSECTS AG3/AG5; FUNGI SCF/SC14 AND PLANTS PR-1.
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CC CC EMBL: M90508; AAA32863.1;
CC CC EMBL: AC005398; AAC69381.1;
CC CC PIR: J01693; J01693.

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DR HSP; P04284; ICEE.
DR InterPro: IPR001283; Allrgn_V5/Tpx1.
DR Pfam: PF00188; SCP; 1.
DR PRINTS: PR000837; V5TPXLIKE.
DR PRODOM: PD000542; Allrgn_V5/Tpx1; 1.
DR SMART: SM00198; SCP; 1.
DR PROSITE: PS01009; SCP_AGS_PRL_SCF_1; 1.
DR PROSITE: PS01010; SCP_AGS_PRL_SCF_2; 1.
KW Plant defense; signal; Pathogenesis-related protein.
FT SIGNAL 1
FT CHAIN 27 161
FT MOD_RES 27 27
FT DISULFID 70 138
FT DISULFID 113 117
FT DISULFID 133 147
FT SEQUENCE 161 AA; 17677 MW; 898B0F6547C3F84 CRC64;

Query Match 8.58; Score 85; DB 1; Length 161;
Best Local Similarity 23.58; Pred. No. 0.81;
Matches 35; Conservative 16; Mismatches 50; Indels 48; Gaps 6;

QY 16 DKREKTELENGTR-----AFANRYTKRKRTWYDCTL-----EEK 53
Db 28 DSPDYLVHNOAGAVGVGMQMDERYAAVARY AEOLRG---NCLHSGGPGENTL 83
QY 54 AKSAKCSPESESEENVYFSAATLNIPLEAGNSWSEIFELRGVYNNKNTSNIAN 113
Db 84 AMGSGDLSG-----VSANVMVSEKANTYMAANTCGVCGHYTO 122
QY 114 MWDSHDKLGCAVDC-SGRTWVCYGP 141
Db 123 VVNRKSVRLGCAKRCNNGTIIICNDYP 151

RESULT 44
PRLC_TOBAC STANDARD: PRT: 168 AA.
AC P09042;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pathogenesis-related protein 1c precursor (PR-1c).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; eusterids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. Samsun NN; TISSUE-Leaf;
RX MEDLINE=90174915; PubMed=2308825;
RA Oshima M., Harada N., Matsuda M., Ohashi Y.;
RA "The nucleotide sequence of pathogenesis-related (PR) 1c protein gene
RA of tobacco."
RA Nucleic Acids Res. 18:182-182(1990).
RN [2]
RP SEQUENCE OF 6-168 FROM N.A.
RC STRAIN-CV. Xanthi;
RX MEDLINE=89041576; PubMed=3186451;
RA Cutt J.R., Dixon D.D., Carr J.P., Klessig D.F.;
RA "Isolation and nucleotide sequence of cDNA clones for the
RA pathogenesis-related proteins PRL1, PRL2 and PRL3 of Nicotiana
RA tabacum cv. Xanthi nc induced by TMV infection."
RA Nucleic Acids Res. 16:9861-9861(1988).
RN [3]
RP SEQUENCE OF 8-168 FROM N.A.
RC STRAIN-CV. Samsun NN;
RX MEDLINE=87231027; PubMed=3295779;
RA Pfitzner U.M., Goodman H.M.;
RA "Isolation and characterization of cDNA clones encoding pathogenesis-
RA related proteins from tobacco mosaic virus infected tobacco plants."
RA Nucleic Acids Res. 15:4449-4445(1987).

```

```

[4]
RN SUBCELLULAR LOCATION.
RP MEDLINE-91224081; PubMed-2026137;
RA Dixon D.C., Cutt J.R., Kleesig D.F.;
RT "Differential targeting of the tobacco PR-1 pathogenesis-related
RT proteins to the extracellular space and vacuoles of crystal
RT idioblasts."
RL EMBL J. 10:1317-1324(1991).
CC -1- FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF PLANTS
CC AGAINST PATHOGENS.
CC SUBCELLULAR LOCATION: ACCUMULATE IN WITHIN THE VACUOLES OF
CC SPECIALIZED CELLS KNOWN AS CRYSTAL IDIOBLASTS.
CC -1- INDUCTION: SYNTHESIZED DURING PATHOGEN INFECTION OR OTHER STRESS-
CC RELATED RESPONSES.
CC -1- PPM: THREE DISULFIDE BONDS ARE PRESENT (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC
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CC
DR EMBL: X17681; CA33666.1; -
DR EMBL: X03454; CA32902.1; -
DR EMBL: X12487; CA31010.1; -
DR PIR: S07580; S07580.
DR HSSP: P04284; ICFE.
DR InterPro: IPR001283; Allrgn_V5/TPX1.
DR Pfam: PF00188; SCP.1.
DR PRINTS: PR00837; V5TPX1.LK.
DR ProDom: PD000542; Allrgn_V5/TPX1.1.
DR SMART: SM00198; SCP.1.
DR PROSITE: PS01009; SCP_AGS_PRL_SC7_1; 1.
DR PROSITE: PS01010; SCP_AGS_PRL_SC7_2; 1.
DR Plant defense; Pathogenesis-related protein; Multigene family; Signal.
FT SIGNAL 1
FT CHAIN 31..168 PATHOGENESIS-RELATED PROTEIN 1C.
SQ SEQUENCE 168 AA; 18583 MW; 2F2F68317C103809 CRC64;

Query Match 8.5%; Score 85; DB 1; Length 168;
Best Local Similarity 21.7%; Pred. No. 0.85;
Matches 38; Conservative 22; Mismatches 51; Indels 64; Gaps 9;

OY 7 CQOREKLDMDREMFTELHNGYR-----AARARYKSKKRMVYDCL-- 50
DB 28 CHAQSQD-----YDAHTARADYVPEPLTWDQVAIAHNTASQ-----LAADCLVH 78
OY 51 -----EKAKYKSAKESPESEENVDVSATLPIPLAONSWMSSTIFELNGKYNK 104
DB 79 SHGQYGEHLAMGSG-----DEFLAA-----KAVEMVYNE-----KQYIAH 113
OY 105 NGKT-----SNIANNVWDSDHDKAGAVDCSGKTHV'-COYGPANAGDKETIY 151
DB 114 DSNFCAQGVCGHYTVVWNSYRVGCAVCCNGGIIVSCNPDNGVYIGKSP 168

RESULT 45
PRIB_TOBAC STANDARD; PRT; 168 AA.
AC P07053;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Pathogenesis-related protein 1B precursor (PR-1B).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Asteridae; eusterids I; Solanales; Solanaceae; Nicotiana.
NCBI_TaxID=4097;

```

```

[1]
RN SEQUENCE FROM N.A.
RP STRAIN-CV, Samson NN; TISSUE-Leaf;
RA MEDLINE-90174914; PubMed-2308824;
RA Oshima M., Harada N., Matsuka M., Ohashi Y.;
RT "The nucleotide sequence of pathogenesis-related (PR) 1b protein gene
RT of tobacco."
RL Nucleic Acids Res. 18:181-181(1990).
RN [2]
RP SEQUENCE FROM N.A.
RP STRAIN-CV, Samson NN;
RA Cornelissen B.J.C., Hooft van Huysdijnen R.A.M., van Loon L.C.;
RA Bol J.F.;
RT Molecular characterization of messenger RNAs for 'pathogenesis-
RT related' proteins 1a, 1b and 1c, induced by TMV infection of
RT tobacco."
RL EMBL J. 5:337-40(1986).
RN [3]
RP SEQUENCE OF 16-168 FROM N.A.
RP STRAIN-CV, Xanthi;
RA MEDLINE-89041576; PubMed-3186451;
RA Cutt J.R., Dixon D.D., Carr J.P., Kleesig D.F.;
RT "Isolation and nucleotide sequence of cDNA clones for the
RT pathogenesis-related proteins Pr1a, Pr1b and Pr1c of Nicotiana
RT tabacum cv. Xanthi nc induced by TMV infection."
RL Nucleic Acids Res. 16:9861-9861(1988).
RN [4]
RN SUBCELLULAR LOCATION.
RP MEDLINE-91224081; PubMed-2026137;
RA Dixon D.C., Cutt J.R., Kleesig D.F.;
RT "Differential targeting of the tobacco PR-1 pathogenesis-related
RT proteins to the extracellular space and vacuoles of crystal
RT idioblasts."
RL EMBL J. 10:1317-1324(1991).
CC -1- FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF PLANTS
CC AGAINST PATHOGENS.
CC SUBCELLULAR LOCATION: ACCUMULATE IN WITHIN THE VACUOLES OF
CC SPECIALIZED CELLS KNOWN AS CRYSTAL IDIOBLASTS.
CC -1- INDUCTION: SYNTHESIZED DURING PATHOGEN INFECTION OR OTHER STRESS-
CC RELATED RESPONSES.
CC -1- PPM: THREE DISULFIDE BONDS ARE PRESENT (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC
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CC
DR EMBL: D90197; BA11221.1; -
DR EMBL: X03465; CA27183.1; -
DR EMBL: X12486; CA31009.1; -
DR EMBL: X17680; CA33665.1; -
DR PIR: B24620; B24620.
DR PIR: S07579; S07579.
DR HSSP: P04284; ICFE.
DR InterPro: IPR001283; Allrgn_V5/TPX1.
DR Pfam: PF00188; SCP.1.
DR PRINTS: PR00837; V5TPX1.LK.
DR ProDom: PD000542; Allrgn_V5/TPX1.1.
DR SMART: SM00198; SCP.1.
DR PROSITE: PS01009; SCP_AGS_PRL_SC7_1; 1.
DR PROSITE: PS01010; SCP_AGS_PRL_SC7_2; 1.
DR Plant defense; Pathogenesis-related protein; Multigene family; Signal.
FT SIGNAL 1
FT CHAIN 31..168 PATHOGENESIS-RELATED PROTEIN 1B.
FT CONFLICT 16..16 S -> A (IN REF. 3).
SQ SEQUENCE 168 AA; 18499 MW; 61FCE3B87AF31F1 CRC64;

Query Match 8.5%; Score 84.5; DB 1; Length 168;

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Best Local Similarity 22.2%; Pred. No. 0.95; Indels 43; Gaps 7;  
Matches 34; Conservative 23; Mismatches 53;

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QY      21 FTLEHNGYR-----AAFAANYKTSKMRMYTDCTLEKAYKSAEKCESEPS 66
      : : | | |
      37 YLDAHNTARADYGVBEPLTWNGVAAYQNY---VSQLAADCNLVHSHGYGENTLAQSG 92
QY      67 SEENVDVFEAATLNIPLEAGSNWSEIFELRGKYRNKNGKT-----SNIANMYWDSH 119
      : : | | |
      93 -----DEMTAA-----KAYEMMYDE-----KQYDHDNSTCAAGGYCGHYTYVWRNS 135
Db
QY      120 DKLGCAVVDGSGKTHYV-CQYGEAKGDKTIY 151
      : : | | |
      136 VRGCAVKNCKNNGYVSCNTPGCVNIGQSPY 168
Db
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Search completed: July 15, 2003, 08:32:41  
Job time : 25 secs

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: July 15, 2003, 08:32:07 ; Search time 80 Seconds  
(without alignments)  
466,182 Million cell updates/sec

Title: US-09-937-555a-2

Perfect score: 997  
Sequence: 1 EGDYSLCOQREKLDLDDMREM.....DYGAGVTCDDDMONLCLIG 181

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: SP\_Archaea:\*  
2: SP\_Bacteria:\*  
3: SP\_Fungi:\*  
4: SP\_Human:\*  
5: SP\_Invertebrate:\*  
6: SP\_Mammal:\*  
7: SP\_Mhc:\*  
8: SP\_Oxigenelle:\*  
9: SP\_Phage:\*  
10: SP\_Plant:\*  
11: SP\_Rodent:\*  
12: SP\_Virus:\*  
13: SP\_Vertebrate:\*  
14: SP\_Unclassified:\*  
15: SP\_Virus:\*  
16: SP\_Bacteriophage:\*  
17: SP\_Archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	997	100.0	181	5	Q962V9
2	290	29.1	274	5	Q16969
3	264.5	26.5	424	5	Q16969
4	264.5	26.5	424	5	Q16969
5	262	26.3	218	5	Q77221
6	261.5	26.2	425	5	Q77221
7	216.5	21.7	465	5	Q9B1P2
8	214	21.5	222	5	Q18519
9	209.5	21.0	246	5	P90958
10	208	20.9	459	5	Q45132
11	207.5	20.8	491	5	Q9B1P2
12	190	19.1	425	5	Q19348
13	189.5	19.0	215	5	Q96317
14	187	18.8	220	5	Q44931
15	184	18.5	224	5	Q9GPN4
16	182	18.3	231	5	Q9B1Q7

17	180	18.1	248	5	Q9B1Q6	Q9B1Q6 cooperia pu
18	178	17.9	248	5	Q9B1Q8	Q9B1Q8 cooperia pu
19	178	17.9	489	11	Q9UJ56	Q9J155 mus musculu
20	178	17.9	489	11	Q9ET66	Q9ET66 mus musculu
21	167	16.8	208	5	Q9B1P2	Q9B1P2 cooperia pu
22	159	15.9	415	4	Q9B1P2	Q9B1P2 cooperia pu
23	158	15.8	500	4	Q9B1P2	Q9B1P2 cooperia pu
24	157	15.7	220	5	Q9B1P2	Q9B1P2 cooperia pu
25	156	15.6	220	5	Q9B1P2	Q9B1P2 cooperia pu
26	154.5	15.5	207	5	Q9B1P2	Q9B1P2 cooperia pu
27	153	15.3	213	5	Q9B1P2	Q9B1P2 cooperia pu
28	152	15.2	212	5	Q9B1P2	Q9B1P2 cooperia pu
29	152	15.2	220	5	Q9B1P2	Q9B1P2 cooperia pu
30	148	14.8	188	11	Q9Z0U6	Q9Z0U6 ratu
31	148	14.8	220	5	Q9B1P2	Q9B1P2 cooperia pu
32	146.5	14.7	208	5	Q9B1P2	Q9B1P2 cooperia pu
33	143.5	14.4	246	5	Q9B1P2	Q9B1P2 cooperia pu
34	143	14.3	207	5	Q9B1P2	Q9B1P2 cooperia pu
35	142	14.2	210	5	Q9B1P2	Q9B1P2 cooperia pu
36	141	14.1	117	5	Q9B1P2	Q9B1P2 cooperia pu
37	141	14.1	208	5	Q9B1P2	Q9B1P2 cooperia pu
38	140.5	14.1	221	5	Q9B1P2	Q9B1P2 cooperia pu
39	140.5	14.1	211	5	Q9B1P2	Q9B1P2 cooperia pu
40	140.5	14.1	332	11	Q9C035	Q9C035
41	140	14.0	434	11	Q9C035	Q9C035
42	139	13.9	462	5	Q9B1P2	Q9B1P2 cooperia pu
43	138.5	13.9	209	5	Q9B1P2	Q9B1P2 cooperia pu
44	137.5	13.8	209	5	Q9B1P2	Q9B1P2 cooperia pu
45	135	13.5	203	4	Q9B1Q8	Q9B1Q8 cooperia pu

## ALIGNMENTS

RESULT 1	Q962V9	PRELIMINARY:	PRT:	181 AA.
ID	Q962V9	01-DEC-2001 (TREMBL)	19, Created	
DR	01-DEC-2001 (TREMBL)	19, Last sequence update		
DT	01-JUN-2002 (TREMBL)	21, Last annotation update		
DE	Platelet inhibitor (Fragment).			
GN	HPI.			
OS	Ancyllostoma caninum (Dog hookworm).			
OC	Eukaryota; Metazoa; Nematoda; Chordata; Rhabdillida; Strongylida;			
OX	Ancyllostomatidae; Ancyllostomatidae; Ancyllostomatidae; Ancyllostoma.			
RN	[1]			
RA	SEQUENCE FROM N. A.			
RT	*Cloning of the hookworm platelet inhibitor (HPI) from adult			
RL	Ancyllostoma caninum.			
DR	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: AF399709; AAK01732.1; --			
DR	InterPro: IPR001283; Allrgn_V5/TPX1.			
DR	ProDom: PD000542; Allrgn_V5/TPX1; 1.			
FT	NOV-TER			
SO	SEQUENCE			
Query Match	181 AA: 2033 MW; FBSCEDEFFE567DNA CRC64;			
Best Local Similarity	100.0%; Score 997; DB 5; Length 181;			
Matches	181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1 EGDYSLCOQREKLDLDDMREMFTLHNGYRAAFARNTSKMTMYDCTLEKAYSAEK 60			
DB	1 EGDYSLCOQREKLDLDDMREMFTLHNGYRAAFARNTSKMTMYDCTLEKAYSAEK 60			
QY	61 CSEERSSEEVVDFSAATINIPLEAGNSWSEIFELRGKVKYKNGKTSNANVMWSDH 120			
DB	61 CSEERSSEEVVDFSAATINIPLEAGNSWSEIFELRGKVKYKNGKTSNANVMWSDH 120			
QY	121 KLGCAVYDCGKTHVCOYGPAAKDGKTIIEGAPCSRSDYGGVTCDDDMONLCLIG 180			

DB 121 KLGCAVVCSCGKTHVVCQYGFPEAKGDKITYEGAPCSKSDYAGVCTDDMDNLICIG 180  
 QY 181 H 181  
 DB 181 H 181

## RESULT 2

ID 016969 PRELIMINARY; PRT; 274 AA.

AC 016969;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Neutrophil inhibitory factor precursor.  
 GN NIF.  
 OS Ancylostoma caninum (Dog hookworm).  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;  
 OC Ancylostomatidae; Ancylostomatidae; Ancylostomatinae; Ancylostoma.  
 OX NCBI\_TaxID=29170;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=HOMOGENATE;  
 RX MEDLINE=94193581; PubMed=7908286;  
 RA Moyle M., Foster D.L., McGrath D.E., Brown S.M., Laroche Y.,  
 de Meuter J., Stanssens P., Bogowitz C.A., Fried V.A., Ely J.A.,  
 Soule H.R., Vlasuk G.P.;  
 RT "A hookworm glycoprotein that inhibits neutrophil function is a ligand  
 of the integrin CD11b/CD18.";  
 RL J. Biol. Chem. 269:10608-10615(1994).  
 DR EMBL: L27427; F00283; F00283; F00283; F00283; F00283; F00283;  
 DR InterPro: I000542; Allrgn\_V5/Tpx1; 1.  
 DR SMART: SM00198; SCP; 1.  
 FT CHAIN  
 FT SIGNAL  
 FT CHAIN  
 SO SEQUENCE 274 AA; 30680 MW; 51580873068DC7E CRC64;

Query Match 29.1%; Score 290; DB 5; Length 274;  
 Best Local Similarity 34.3%; Pred. No. 4.4e-19;

Matches 69; Conservative 23; Mismatches 57; Indels 52; Gaps 7;

QY 14 DDDREMFTELHNGYFAFAFARNY-----KTSKRTMYDCTL 50  
 DB 35 NDSRIQFLAMHNGYSKLALGHISTESESDDDDGFLDPFAPRAKRYLEYDCEA 94  
 QY 51 EKKAVKSKKCESE---PSEENVDPVSAATLNI---PLEAGNSWSEIFEL-----R 98  
 DB 95 EKSAYMSARNCSDSSPPEGIDENKTYIPENS-NISEALAKAMISMAKFAFNLKTKEGE 153  
 QY 99 GKVYKKNKTSNINANVWDSHDKLCAVYDC-----SGKT-----HVVCOYGE 142  
 DB 154 GVLVRSNNDISNFMANLAMDAREKFCACAVVNCPLGEIDDETNDGETYATITIHVCHYFKI 213  
 QY 143 AKGDGKTYEGAPCSKSDY 163  
 DB 214 NRTGQPIYKVGTPCDDCSRY 234

## RESULT 3

ID 076744 PRELIMINARY; PRT; 424 AA.

AC 076744;  
 DT 01-NOV-1998 (TREMBLrel. 08, Created)  
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Ancylostoma secreted protein 1 precursor.  
 GN ASP1.  
 OS Necator americanus.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;  
 OC Ancylostomatidae; Ancylostomatidae; Bunostominae; Necator.  
 OX NCBI\_TaxID=51031;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SHANGHAI;  
 RX MEDLINE=96215086; PubMed=8636085;  
 RA Hawdon J.M., Jones B.E., Hoffman D.R., Hotez P.J.;  
 RT "Cloning and characterization of Ancylostoma-secreted protein. A novel  
 protein associated with the transition to parasitism by infective  
 hookworm larvae.";  
 RT hookworm larvae.";  
 RT J. Biol. Chem. 271:6672-6678(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SHANGHAI;  
 RX MEDLINE=8915177;  
 RA Bin L., Hawdon J., Qiang S., Hainan R., Huifeng Q., Wei H.,  
 Zhu L., Xiang L., Xing F., Zheng F., Hotez P.;  
 RA "Ancylostoma secreted protein 1 (ASP-1) homologues in human  
 hookworms.";  
 RT Mol. Biochem. Parasitol. 98:143-149(1999).  
 DR EMBL: AF079521; AAD13340.1; -;  
 DR HSSP: P04284; 1CPE.  
 DR InterPro: IPR001283; Allrgn\_V5/Tpx1.  
 DR Pfam: PF00188; SCP; 1.  
 DR PRINTS: PR00837; V5TPXLIKE.  
 DR PRODOM: PD000542; Allrgn\_V5/Tpx1; 2.  
 DR SMART: SM00198; SCP; 2.  
 FT SIGNAL  
 FT CHAIN  
 FT CHAIN  
 SO SEQUENCE 424 AA; 45742 MW; BFLB2P95F9B49F CRC64;

Query Match 26.5%; Score 264.5; DB 5; Length 424;  
 Best Local Similarity 32.5%; Pred. No. 1.8e-16;

Matches 62; Conservative 27; Mismatches 71; Indels 31; Gaps 6;

QY 7 CQGREKIDDDMEFMTELHNGYFAFAFARNY-----KTSKRTMYDCTLEKAYK 56  
 DB 227 CPSNTGMDVSVDHDFLVSHPNSVAKGLEPDLGCAKAKAKAKMYDDEVASAIR 286  
 QY 57 SAEKCEPSSSEED---NDVFSAAATLNI---PLEAGNSWSEIFEL-----LRG 99  
 DB 287 HGKCYOQSHSEDPGLGENTIKTSYLKFDKNKAQASQAMWNLKEKYGSPNSVLT 346  
 QY 100 KYINR-NGKTSNINANVWDSHDKLCAVYDCSGKTHVVCQYGFPEAKGDKITYEGAPCS 158  
 DB 347 ALMNRFMQIGHYTOAMADITYKLCAVYFCNDTFGVCQYGPQGNMGHVIYTMGPCS 406  
 QY 159 RCDYGAQYTC 169  
 DB 407 QCS---PQATC 414

## RESULT 4

ID 09X441 PRELIMINARY; PRT; 424 AA.

AC 09X441;  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Ancylostoma secreted protein 1 precursor.  
 GN ASP1.  
 OS Ancylostoma caninum (Dog hookworm).  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;  
 OC Ancylostomatidae; Ancylostomatidae; Ancylostomatinae; Ancylostoma.  
 OX NCBI\_TaxID=29170;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SHANGHAI;  
 RX MEDLINE=20163524; PubMed=10701589;  
 RA Shan Q., Zhan B., Xiao S.-H., Feng Z., Hotez P., Hawdon J.M.;  
 RT "Variation between ASP-1 molecules from Ancylostoma caninum in China  
 and the United States.";  
 RT J. Parasitol. 86:181-185(2000).  
 DR EMBL: AF132291; AAD31839.1; -;  
 DR HSSP: P04284; 1CPE.



```

DR InterPro: IPR001283; Allrgn_V5/Tpx1.
DR Pfam: PF00188; SCP, 1.
DR PRINTS: PR00837; V5TPX1KE.
DR PRODOM: PD000542; Allrgn_V5/Tpx1; 2.
DR SMART: SM00198; SCP, 2.
FW SIGNAL.
FT CHAIN 1 18 POTENTIAL.
SQ SEQUENCE 424 AA; 45761 MW; 8409CDF8AEDCD48E CRC64;

Query Match
Best Local Similarity 26.5%; Score 264.5; DB 5; Length 424;
Matches 62; Conservative 27; Mismatches 71; Indels 31; Gaps 6;

OY 7 COOREKLDDBREMFTELHNGYRAAFARNY-----KTSKRTWVYDCTLEEKAYK 56
DB 227 CPSTNGMTDSVDRDTFLSVHNEFRSSVARGLEPDALGNAAPKAAKRLKMYDCEVEASAIR 286
OY 57 SAEKSEEPSESE-----NVDFSAATLNI-----PLEAGNSWSEIFE-----LRG 99
DB 287 HGNCVYQHSHGDRGLGLENIKTSYVAKEDKNAKAKOSQWMLNELKGYGSPSNVLT 346
OY 100 KYNKNG-KTSINANWYDSDHKLGCAYVDCSGKTHVYCYGPEAKGDKITYEGAPCS 158
DB 347 ALMKRPMQIGHITTOAMDTTILGCAVYFCNDFTGVCQYGPNGYNGHVITTMGQPCS 406
OY 159 RCDSDYAGGYTC 169
DB 407 QCS---PGATC 414

RESULT 5
OY 077221 PRELIMINARY; PRT; 218 AA.
DB 077221:
OY 01-NOV-1998 (TREMBLrel. 08, Created)
OY 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
OY 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Secreted protein ASP-2 precursor.
GN ASP-2.
OS Ancylostoma caninum (Dog hookworm).
OC Eukaryota; Metazoa; Nematoda; Chromodorea; Rhabditiida; Strongyliida;
OC Ancylostomatidae; Ancylostomatidae; Ancylostomatinae; Ancylostoma.
OX NCBI_TaxID=29170;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALTIMORE;
RX MEDLINE-99270306; PubMed-10340481;
RA Hawdon J.M., Narsisimhan S., Hoter P.J.;
RT Ancylostoma secreted protein 2: cloning and characterization of a
RT second member of a family of nematode secreted proteins from
RT Ancylostoma caninum.
RL Mol. Biochem. Parasitol. 99:149-165(1999).
DR HSP, P04284; ICFE;
DR HSP, P04284; ICFE;
DR InterPro: IPR001283; Allrgn_V5/Tpx1.
DR Pfam: PF00188; SCP, 1.
DR PRINTS: PR00837; V5TPX1KE.
DR PRODOM: PD000542; Allrgn_V5/Tpx1; 1.
DR SMART: SM00198; SCP, 1.
DR PROSITE: PS01009; SCP_AGS_PRL_SCT_1; 1.
FW SIGNAL.
FT CHAIN 1 18 POTENTIAL.
SQ SEQUENCE 218 AA; 23954 MW; 8C263DEA808AA6F CRC64;

Query Match
Best Local Similarity 26.3%; Score 262; DB 5; Length 218;
Matches 58; Conservative 38; Mismatches 69; Indels 26; Gaps 5;

OY 13 LDDMKEMFTELHNGYRAAFARNY-----KTSKRTWVYDCTLEEKAYKSGCS 62
DB 27 MTEARQKFLVDHNSYRSMYAKGAKDAISGNAPFAAKKMKITIDCAVESTANQNAKCY 86

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OY 63 EEPSESE---ENVDFSAATLNI-----PLEAGNSWSEIFE-----ELGKYNNKNGT 108
DB 87 FAHSHRGVGENEMNSTARQMDKAAQAAQASDQNFSELAKEKYGOENKLTTLNNGVNI 146
OY 109 SNINANWYDSDHKLGCAYVDCSGKTHVYCYGPEAKGDKITYEGAPCSRGSDYAGYT 168
DB 147 GHYQWYQWQESKICLCYENCSMTITGYCYSQGMNMSLITENGNPCTKIDSDCSNNS 206
OY 169 CDDPMQMLACI 179
DB 207 CSAG--EALCV 215

RESULT 6
OY 077153 PRELIMINARY; PRT; 425 AA.
DB 077153:
OY 01-NOV-1998 (TREMBLrel. 08, Created)
OY 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
OY 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Ancylostoma-secreted protein 1 precursor.
GN Asp1.
OS Ancylostoma duodenale.
OC Eukaryota; Metazoa; Nematoda; Chromodorea; Rhabditiida; Strongyliida;
OC Ancylostomatidae; Ancylostomatidae; Ancylostomatinae; Ancylostoma.
OX NCBI_TaxID=51022;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SHANGHAI;
RX MEDLINE-96215086; PubMed-8636085;
RA Hawdon J.M., Jones B.F., Hoffman D.R., Hoter P.J.;
RT Cloning and characterization of Ancylostoma-secreted protein. A novel
RT protein associated with the transition to parasitism by infective
RT hookworm larvae.
RL J. Biol. Chem. 271:6672-6678(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-SHANGHAI;
RX MEDLINE-9915177;
RA Bin Z., Hawdon J., Qiang S., Hainan R., Huang Q., Wei H.,
RA Shu-Hua X., Fiehua L., Xing G., Zheng F., Hoter P.;
RT Ancylostoma secreted protein 1 (ASP-1) homologues in human
RT hookworms.
RL Mol. Biochem. Parasitol. 98:143-149(1999).
DR EMBL: AF074602; AAD1339.1;
DR InterPro: IPR001283; Allrgn_V5/Tpx1.
DR Pfam: PF00188; SCP, 1.
DR PRINTS: PR00837; V5TPX1KE.
DR PRODOM: PD000542; Allrgn_V5/Tpx1; 2.
DR SMART: SM00198; SCP, 2.
FW SIGNAL.
FT CHAIN 1 19 POTENTIAL.
SQ SEQUENCE 425 AA; 45821 MW; 1F6B9D7E62EEDDAB CRC64;

Query Match
Best Local Similarity 26.2%; Score 261.5; DB 5; Length 425;
Matches 64; Conservative 23; Mismatches 73; Indels 31; Gaps 6;

OY 7 COOREKLDDBREMFTELHNGYRAAFARNY-----KTSKRTWVYDCTLEEKAYK 56
DB 228 CPSTNGMTDSVDRDTFLSVHNEFRSSVARGLEPDALGNAAPKAAKRLKMYDCEVEASAIR 287
OY 57 SAEKSEEPSESE-----ENVDFSAATLNI-----PLEAGNSWSEIFE-----LRG 99
DB 288 HGNCVYQHSHGDRGLGLENIKTSYVAKEDKNAKAKOSQWMLNELKGYGSPSNVLT 347
OY 100 KYNKNG-KTSINANWYDSDHKLGCAYVDCSGKTHVYCYGPEAKGDKITYEGAPCS 158
DB 348 ALMKRPMQIGHITTOAMDTTILGCAVYFCNDFTGVCQYGPNGYNGHVITTMGQPCS 407
OY 159 RCDSDYAGGYTC 169

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DB      408 GCA---ATATC 415

RESULT 7
ID      0981P2      PRELIMINARY:      PRT:      465 AA.
AC      0981P2;
DT      01-JUN-2001 (TREMblrel. 17, Created)
DT      01-JUN-2001 (TREMblrel. 17, Last sequence update)
DE      01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE      Activation associated secreted protein-like protein (Fragment).
OS      Cooperia punctata.
OC      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
OC      Trichostrongyloidea; Cooperiidae; Cooperia.
OX      NCBI_TaxID=96640;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=CP-ASP-1B;
RA      Yacuda A.P., Eysker M., Vieira Bressan M.C.R., De Vries E.;
RT      "Analysis of a family of activation associated protein (ASP)
RT      homologs of Cooperia punctata.";
RL      Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF352714; AKK3199.1; -.
DR      HSSP; P04284; 1CFE.
DR      InterPro; IPR001283; Allrgn_V5/Tpx1.
DR      Pfam; PF00188; SCP; 1.
DR      PRINTS; PR00837; V5TPX1KE.
DR      PRODOM; PD000542; Allrgn_V5/Tpx1; 2.
DR      SMART; SM00198; SCP; 1.
DR      NON_TER
SQ      SEQUENCE 465 AA; 51628 MW; F00F886C2A99993A CRC64;

Query Match      21.7%; Score 216.5; DB 5; Length 465;
Best Local Similarity 27.8%; Pred. No. 5.9e-12;
Matches 57; Conservative 30; Mismatches 79; Indels 39; Gaps 7;

OY      5 SLCQOREKIDDDREMEFTELHNGYRAAFARNY-----RTSKRTMYDCTLEEK 53
DB      15 ALLSLNNGTDEVRFLFLDKHNEYSRLVAKGAPNPVEGNTSRRAALMLVRIODEVED 74
OY      15 AYKSAE-KCSEPPSEEE-----NVDFSAATLNIPLDAGNSWSEIFELRG- 99
DB      75 MMTMAQOCAYAPFESDKHYGRNTMGIPNKTAAESSV-----DWFED---ELRSY 126
OY      100 -----KVYKNGKTSNTIANWVDSHDKLCAVVDSCGKTHVVCQYGEAKGDGKTYE 154
DB      127 GVPDNRKTYRNIDAYDYSQWYQNSYKIGCVVASCSSMTWVACGSPAGNDSLIYE 186
OY      155 APCSRCSYDCAVCTDDDMQNLICI 179
DB      187 DPCMKNECKC-TNCTCKGKALCI 210

RESULT 8
ID      018519      PRELIMINARY:      PRT:      222 AA.
AC      018519;
DT      01-JAN-1998 (TREMblrel. 05, Created)
DT      01-JAN-1998 (TREMblrel. 05, Last sequence update)
DT      01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE      24 kDa excretory/secretory protein.
OS      Haemonchus contortus (Barber pole worm).
OC      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
OC      Trichostrongyloidea; Haemonchidae; Haemonchus.
OX      NCBI_TaxID=6289;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      MEDLINE-97418804; PubMed-9274880;
RA      Schalling H.D., van Leeuwen M.A., Verstegen B.E., Cornelissen A.M.;
RT      "Molecular characterization and expression of two putative protective
RT      excretory secretory proteins of Haemonchus contortus.";
RL      Mol. Biochem. Parasitol. 88:203-213(1997).

DB      EMBL; U64793; AAC47714.1; -.
DR      InterPro; IPR001283; Allrgn_V5/Tpx1.
DR      Pfam; PF00188; SCP; 1.
DR      PRINTS; PR00837; V5TPX1KE.
DR      PRODOM; PD000542; Allrgn_V5/Tpx1; 1.
DR      SMART; SM00198; SCP; 1.
DR      PROSITE; PS01009; SCP_AGS_PRL_SCP_1; 1.
SQ      SEQUENCE 222 AA; 24633 MW; 37B8840ED83100D8 CRC64;

Query Match      21.5%; Score 214; DB 5; Length 222;
Best Local Similarity 28.0%; Pred. No. 4.1e-12;
Matches 58; Conservative 28; Mismatches 89; Indels 32; Gaps 8;

OY      2 GYSLCQOREKIDDDREMEFTELHNGYRAAFARNY-----RTSKRTMYDCT 49
DB      17 GHASWCPTNGMSDEVQGFVKNHNAHYTLVAKGEAKNAKEIGYAPRAAHLKYVDCA 76
OY      50 LERKAYKSAEKC--SEPPSEEE--VDVFSATLN-----IPLDAGNSWSEIFELRG 100
DB      77 IETNMFNFAKCVAFANYSSESNMNGOYLWYTSILNOKTVAAESVDLWFDL-QONGV 135
OY      101 VYNK-----NGKTSIANWVDSHDKLCAVVDSCGKTHVVCQYGEAKGDGKTYE 153
DB      136 PYDNVMTAVFNNGVHYGYQVWQSKNIGCAVEMCSDMTFVACETDSAGVYKMPLEY 195
OY      154 GPCSRCSYDCAVCTDDDMQNLICI 179
DB      196 GNPCTNNECKCINVCSPD--EALCI 220

RESULT 9
ID      P90958      PRELIMINARY:      PRT:      246 AA.
AC      P90958;
DT      01-MAY-1997 (TREMblrel. 03, Created)
DT      01-MAY-1997 (TREMblrel. 03, Last sequence update)
DT      01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE      T05A10.5 protein.
OS      Caenorhabditis elegans.
OC      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC      Rhabditidae; Pelodierinae; Caenorhabditis.
OX      NCBI_TaxID=6239;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      Sultson J.E.;
RA      Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RL      [2]
RN      MEDLINE-99069613; PubMed-9851916;
SQ      SEQUENCE 246 AA; 27956 MW; FB5770261350DE54 CRC64;

Query Match      21.0%; Score 209.5; DB 5; Length 246;
Best Local Similarity 27.2%; Pred. No. 1.2e-11;
Matches 59; Conservative 26; Mismatches 87; Indels 45; Gaps 7;

OY      6 LCOQREKIDDD-----RMEFTELHNGYRAAFARNY-----RTSK 40
DB      29 LQAQSMYKDDGSGFOCDNSLVSDVTRNFTLEQHNFYRSLAAGFMWGTNTSQPASQ 88
OY      41 KMTWYDCTLEEKYKSAEKC-----SEPPSEEEVDVFSAT--LNIPLDAGNSW 91

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DB 89 MIKREYCMLEPROMNANNCVFAHSAHYERPNOCNTMSSFSNPDRLIHTAVEKMW 148
QY 92 SEIFE-----LRKYVKNKGT-SNIAMWDSHDLGCAVYDSCGKTHVCOXGPE 142
DB 149 CELEFPCTIDNVLTPLELMDLKGKALIGHYQGMNDRTYLGSGIANCPKMSYVCHYGRF 208
QY 143 AKGCKTIEEGAPSCSCSDYAGVTCDDQMLICI 179
DB 209 GNRKNNKIYELGPCVDDCDIGVDCER--TTSICV 243

RESULT 10
ID 045132 PRELIMINARY; PRT; 459 AA.
AC 045132;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Putative secretory protein precursor.
GN HC40.
OS Haemochus contortus (Barber pole worm).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
OC Trichostrongyloidea; Haemonchidae; Haemonchinae; Haemonchus.
CX NCBI_TaxID=6289;
RN [1]
RP SEQUENCE FROM N.A.
RA Rehman A., Jaamer D.P.;
RL Submitted (FEB-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF047417; AAC03562.1;
DR InterPro; IPR001283; Allrgn_V5/Trpx1.
DR Pfam; PF00188; SCP; 1.
DR PRINTS; PR00837; V5TPXLIKE.
DR PRODOM; PD000542; Allrgn_V5/Trpx1; 2.
DR SMART; SM00198; SCP; 2.
KW SIGNAL.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 459 AA; 50924 MW; 88FAC09A01FC57B CRC64;

Query Match 20.9%; Score 208; DB 5; Length 459;
Best Local Similarity 28.5%; Pred. No. 3,6e-11;
Matches 35; Conservative 36; Mismatches 74; Indels 28; Gaps 8;

QY 13 LDDNREHRETELNGYRAAFARN-----KTSKRTMYDCTLEKAYKSAEKS 62
DB 267 MIDEAKMEVDNHNENSLIKQAGKRGCFAPFAAMKMYNTDCDVANMMSKTCI 326
QY 63 EEPSESE-----ENVDFSAATLN--IPRAGSMSEIFEL--RGRVKNKGT-- 108
DB 327 FGLNTAAMLKRWGNMNMMSKANNTTEAARAVAMWPGDLOKGVPENNVFTMVTTL 386
QY 109 SNIAMWDSHDLGCAVYDSCGKTHVCOXGPEAKGDKTIYEGAPSCSCSYGA-G 166
DB 387 SKISQAMOSSRICQVYPCMSMTVYCEIRNPGGLPGALITVDVDDPTDADOCQPG 446
QY 167 VTCDQDQMLICI 179
DB 447 CTCGRD--EALCV 457

RESULT 11
ID 09104 PRELIMINARY; PRT; 491 AA.
AC 09104;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Activation associated secreted protein-like protein (Fragment).
OS Cooperia punctata.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
OC Trichostrongyloidea; Cooperiidae; Cooperia.
CX NCBI_TaxID=96640;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN-CP-ASP-1A;
RA Yatsuda A.P., Eysker M., Vletra Bressan M.C.R., De Vries E.;
RT "Analysis of a family of activation associated secreted protein (ASP)
RL homologs of Cooperia punctata."
DB Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF352702; AA35187.1;
DR InterPro; IPR001283; Allrgn_V5/Trpx1.
DR InterPro; IPR002965; P-rich-extendn.
DR Pfam; PF00188; SCP; 1.
DR PRINTS; PRO1217; PRICEXTENS.
DR PRODOM; PD000542; Allrgn_V5/Trpx1; 2.
DR SMART; SM00198; SCP; 2.
DR PROSITE; PS01009; SCP_AGS_PRL_SCT_1; 1.
FT NON_TER.
SQ SEQUENCE 491 AA; 55244 MW; 25B9B435E613857E CRC64;

Query Match 20.8%; Score 207.5; DB 5; Length 491;
Best Local Similarity 28.9%; Pred. No. 4,4e-11;
Matches 57; Conservative 30; Mismatches 85; Indels 25; Gaps 8;

QY 6 LCQOREKLDNREHRETELNGYRAAFARN-----YKTSKRTMYDCTLEK 54
DB 12 TCSLNGMTVYIKRITLDNHNENSLVNRGAKDPRTGOTIPKATRLMKSYDCEADVY 71
QY 55 YKSAE-KC--SEEPSESEENVDFSAATLNIP--ENGNS---HMSSEIFEL--RGRVKN 103
DB 72 MNMAQACQATYRKSKKRNNTGICIRFNKKAESYVDNFNIRYGVPRDMYT 131
QY 104 KNGTSMIAMWDSHDLGCAVYDSCGKTHVCOXGPEAKGDKTIYEGAPSCSCSY 163
DB 132 RDTSEVYSGIIMQDSYKRGCAVAMCQSMTWACAVNPAGNNGYSGIYEGEPCRNOC 191
QY 164 GA-GVTCDDQDQMLICI 179
DB 192 KNCQCTCT--TESICT 206

RESULT 12
ID 019348 PRELIMINARY; PRT; 425 AA.
AC 019348;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE FilC7.3 protein.
GN FilC7.3 OR VAP-1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
CX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-BRISTOL N2;
RC MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Alnsough R., Anderson K., Baynes C., Berks M., Coulson A.,
RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Fulton L.,
RA Crahan M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kerhaw J., Kirsten J., Laister N., Latreille P., Loman M.,
RA Lightning J., Lloyd C., Murray A., Mortimore B., O'Brien M.,
RA Parsons J., Smith A., Sonnenhauser E., Staden R., Sulston J.,
RA Smalton N., Smit A., Thompson K., Thompson K., Vaughan K., Waterston R.,
RA Thierly-Mieg J., Thomas K., Winkler-Sproat J., Wolfdmeyer P.,
RA Watson A., Wellstock L., Wilkinson-Sproat J., Wolfdmeyer P.,
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RL elegans."
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN-BRISTOL N2;
RA Tatch A., Vetter J.;

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RT  EMBL: AF314563; Paraetol. 109:91-99(2000).
DR  InterPro: IPR001283; Allrgn_V5/TpX1.
DR  Pfam: PF00188; SCP; 1.
DR  PRINTS: PR00837; V5TPX1KE.
DR  ProDom: PD000542; Allrgn_V5/TpX1; 1.
DR  SMART: SM00198; SCP; 1.
SQ  SEQUENCE 224 AA; 25253 MW; 8AF47A015225C3A CRC64;

Query Match      18.5%; Score 184; DB 5; Length 224;
Best Local Similarity 30.3%; Pred. No. 2.6e-09;
Matches 57; Conservative 20; Mismatches 73; Indels 38; Gaps 9;

QY  10 REKIDDMREMTLENGYRAAFAR-NKTS-----KRTVYDCLEEKAYKSE 59
DB  21 RGLTLPOYREKRYREHNRLRSKLAGYKNSAGKMPKGNMEKNCCELEMAORMD 80
QY  60 KCSPEPSEEE-----NDVFSATNILEAGNSWSEIF-ELRGKYN 103
DB  81 QCVGNSPKRBRGRIGENYTORSDTSVAVYGSIMALE---SMVVELRSTKKNPS 137
QY  104 K-----NGKTSNIAMVWDSHDKGCAV-VDC-SGKTHV-VCQYGPRAKDGKTYIEEG 154
DB  138 KYSIVANRGVSNFTQJLNGKTKYVGGIATHCDSGRATFAVAVCOYINPEGNTSESYIEG 197
QY  155 APCSRCD 162
DB  198 RPKCTDMD 205

RESULT 16
QY  09BI07 PRELIMINARY; PRT; 231 AA.
AC  09BI07;
DT  01-JUN-2001 (TrEMBLrel. 17, Created)
DT  01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT  01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE  Activation associated secreted protein-like protein (Fragment).
OS  Cooperia punctata.
OC  Eukaryota; Metazoa; Nematoda; Chromodorea; Rhabditida; Strongyliida;
OC  Trichostrongyloidea; Cooperiidae; Cooperia.
OX  NCBI_TaxID=96640;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN-CP-ASPVAR-5;
RA  Yatsuda A.P., Eysker M., Vieira Bressan M.C.R., De Vries E.;
RT  Analysis of a family of activation associated secreted protein (ASP)
RT  homologs of Cooperia punctata.
RT  Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RL  EMBL: AF352699; AAK35184.1; -.
DR  HSSP: P04284; ICPE.
DR  InterPro: IPR001283; Allrgn_V5/TpX1.
DR  Pfam: PF00188; SCP; 1.
DR  PRINTS: PR00837; V5TPX1KE.
DR  ProDom: PD000542; Allrgn_V5/TpX1; 1.
DR  SMART: SM00198; SCP; 1.
FT  NON_TER 1
SQ  SEQUENCE 231 AA; 25824 MW; C5225C9AA17AD00 CRC64;

Query Match      18.3%; Score 182; DB 5; Length 231;
Best Local Similarity 26.6%; Pred. No. 4.1e-09;
Matches 53; Conservative 27; Mismatches 86; Indels 36; Gaps 7;

QY  7 COOREKLDMDREMTLENGYRAAFARNY-----KTSKRTVYDCLEEKAYK 57
DB  32 CTANNGMTDVRQVYLDKHNERYQLVARGEAOKTGFAPKAARHLRLRYDCDLEAHVMEH 91
QY  58 AEKCSPEPSEEE-----EENVDVSATNILEAGNSWSEIFELRGKYN 103
DB  92 VKTKCGHSPFVLKRGONIMATVNPNDKAAKRSV-----DMYIELTKYGITADN 146
QY  104 K-----NGKTSNIAMVWDSHDKGCAVDC--SGKTHVVCQYGPRAKDGKTYIEEGAP 156

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DB  147 KISIDNAATGHSQVWQKSNRLGCAVSCPEORLTFVGEYLPNGNTLRHLIYDIGEP 206
QY  157 CSRCSDYAGVTCDDDMONLICI 179
DB  207 CKRDECKCS-SCRCSTOLSMCI 228

RESULT 17
QY  09BI06 PRELIMINARY; PRT; 248 AA.
AC  09BI06;
DT  01-JUN-2001 (TrEMBLrel. 17, Created)
DT  01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT  01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE  Activation associated secreted protein-like protein (Fragment).
OS  Cooperia punctata.
OC  Eukaryota; Metazoa; Nematoda; Chromodorea; Rhabditida; Strongyliida;
OC  Trichostrongyloidea; Cooperiidae; Cooperia.
OX  NCBI_TaxID=96640;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN-CP-ASPVAR-5;
RA  Yatsuda A.P., Eysker M., Vieira Bressan M.C.R., De Vries E.;
RT  Analysis of a family of activation associated secreted protein (ASP)
RT  homologs of Cooperia punctata.
RT  Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RL  EMBL: AF352700; AAK35185.1; -.
DR  HSSP: P04284; ICPE.
DR  InterPro: IPR001283; Allrgn_V5/TpX1.
DR  Pfam: PF00188; SCP; 1.
DR  PRINTS: PR00837; V5TPX1KE.
DR  ProDom: PD000542; Allrgn_V5/TpX1; 1.
DR  SMART: SM00198; SCP; 1.
FT  NON_TER 1
SQ  SEQUENCE 248 AA; 27528 MW; ABF932E60DB67411 CRC64;

Query Match      18.1%; Score 180; DB 5; Length 248;
Best Local Similarity 26.1%; Pred. No. 6.8e-09;
Matches 53; Conservative 28; Mismatches 86; Indels 36; Gaps 6;

QY  7 COOREKLDMDREMTLENGYRAAFARNYKTSK-----MTVYDCLEEKAYK 57
DB  49 CTIDNGMTDEARQVFLKHNERYQLVARGEAOKTGAPPAARLRLKRYDCDLEAHVMEH 108
QY  58 AEKCSPEPSEEE-----EENVDVSATNILEAGNSWSEIFELRGKYN 103
DB  109 VAKCKGHSHTEDVYKRGONIMATVNPNDKAAKRSV-----DMYIELTKYGITADN 163
QY  104 K-----NGKTSNIAMVWDSHDKGCAVDC--SGKTHVVCQYGPRAKDGKTYIEEGAP 156
DB  164 KISIDNAATGHSQVWQKSNRLGCAVSCPEORLTFVGEYLPNGNTLRHLIYDIGEP 223
QY  157 CSRCSDYAGVTCDDDMONLICI 179
DB  224 CKRDECKCS-SCRCSTOLSMCI 245

RESULT 18
QY  09BI08 PRELIMINARY; PRT; 248 AA.
AC  09BI08;
DT  01-JUN-2001 (TrEMBLrel. 17, Created)
DT  01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT  01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE  Activation associated secreted protein-like protein (Fragment).
OS  Cooperia punctata.
OC  Eukaryota; Metazoa; Nematoda; Chromodorea; Rhabditida; Strongyliida;
OC  Trichostrongyloidea; Cooperiidae; Cooperia.
OX  NCBI_TaxID=96640;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN-CP-ASPVAR-7;
RA  Yatsuda A.P., Eysker M., Vieira Bressan M.C.R., De Vries E.;

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\*Analysis of a family of activation associated secreted protein (ASP)  
 RT homologs of Cooperia punctata.  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF552898; AKK35183.1;  
 DR HSSP: P04284; 1CFE.  
 DR InterPro: IPR001283; Allrgn\_V5/tpx1.  
 DR Pfam: PF00188; SCP; 1.  
 DR PRINTS: PR00837; V5TPXLIKE.  
 DR PRODOM: PD000542; Allrgn\_V5/tpx1; 1.  
 DR SMART: SM00198; SCP; 1.  
 FT NON\_TER  
 SQ SEQUENCE 248 AA; 27558 MW; A7ED083B9BEF7481 CRC64;

Query Match 17.98; Score 178; DB 5; Length 248;  
 Best Local Similarity 26.18; Pred No. 1e-08; 87; Indels 36; Gaps 6;  
 Matches 53; Conservative

QY 7 COORELDDMEETELANGYRAAFARNYTKS-----RTWVYDCTLEEKAYKS 57  
 DB 49 CTLDNGMTDEANQVLDKNEYRLVARGAQNKTGLAPPAKRLKRYDCDLEAHVMEH 108  
 QY 58 AEEGSEBSESE-----ENVDVSAATINIPLEAGNSWSEIFELRGKYN 103  
 DB 109 VAKCKGSHPEVYLGKRGQNTMAITYNLDKAAKRSV-----DMYFELTYGTDN 163  
 QY 104 K-----NGETSNIAWMDSHDKGCAVYDC--SGTHVCOYGPPEAKGKTYEEGAP 156  
 DB 164 KISIDNAATGHYSQVYVQKSNRIGCAAVSCPEQRRLTYGCEYVPGGNTLRHLITYDIGEP 223  
 QY 157 CSKCSDYGAGVYCDDDQNTLCI 179  
 DB 224 CKRDECKCS-SCRCSTLSMCI 245

RESULT 19  
 ID 09J156 PRELIMINARY; PRT; 489 AA.  
 AC 09J156;  
 DT 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, last annotation update)  
 DE Cysteine-rich protease inhibitor.  
 GN 1200009H1IRIK OR CRPI.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Jang J.S., Hahn Y., Chung J.H.;  
 RT "Identification of novel mouse cytoskeleton-rich protease inhibitor  
 gene."  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB046537; BAB03398.1;  
 DR HSSP: P04284; 1CFE.  
 DR MGD: MGI:1921366; 1200009H1IRIK.  
 DR InterPro: IPR001283; Allrgn\_V5/tpx1.  
 DR Pfam: PF00188; SCP; 1.  
 DR PRINTS: PR00837; V5TPXLIKE.  
 DR PRODOM: PD000542; Allrgn\_V5/tpx1; 1.  
 DR SMART: SM00198; SCP; 1.  
 DR PROSITE: PS01009; SCP\_AGS\_PRL\_SG7\_1; 1.  
 DR PROSITE: PS01010; SCP\_AGS\_PRL\_SG7\_2; 1.  
 KW Protease.  
 SQ SEQUENCE 489 AA; 52676 MW; 01C07BE12E3C9D CRC64;

Query Match 17.98; Score 178; DB 11; Length 489;  
 Best Local Similarity 28.68; Pred. No. 2.4e-08;  
 Matches 53; Conservative 25; Mismatches 73; Indels 34; Gaps 9;  
 QY 13 LDDDMREMTLHNGYRAAFARNYTSKRTWYDCTLEEKAYKSARK-----SEEPSE 68  
 DB 21 LTDEKQTMVLDLHNGYRAOVSP--PASDMLQHRWDELLAFAFAKAYQKCVGHKNGRGR 78

QY 69 EENVDFSAATINIPLEAGNSWSEIFELRGKYN-----KNGKTSNIAWMDSHDK 121  
 DB 79 GENLEAATIDEGMDVPLAVGN--WHEHE-----YNNSTATCDPNMCGHYTVWMSKTER 132  
 QY 122 LGCAVYDC-----SGKTH-VVCOYGPPEAKGDKTYEEGAPCSGSDYAGVYCDDDM 173  
 DB 133 ICGSHFCETLQGEVEMANHLVNCYEPGPNVNGRKRPYDGTGSCPCP---LGYSK----- 185  
 QY 174 ONLTC 178  
 DB 186 ENSLC 190

RESULT 20  
 ID 09ET66 PRELIMINARY; PRT; 489 AA.  
 AC 09ET66;  
 DT 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, last annotation update)  
 DE Cysteine-rich protease inhibitor.  
 GN CRPI.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Jang J.S., Hahn Y., Chung J.H.;  
 RT "Genomic structure of murine cytoskeleton-rich protease inhibitor gene."  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AB046538; BAB03453.1; JOINED.  
 DR HSSP: P04284; 1CFE.  
 DR InterPro: IPR001283; Allrgn\_V5/tpx1.  
 DR Pfam: PF00188; SCP; 1.  
 DR PRINTS: PR00837; V5TPXLIKE.  
 DR PRODOM: PD000542; Allrgn\_V5/tpx1; 1.  
 DR SMART: SM00198; SCP; 1.  
 DR PROSITE: PS01009; SCP\_AGS\_PRL\_SG7\_1; 1.  
 DR PROSITE: PS01010; SCP\_AGS\_PRL\_SG7\_2; 1.  
 KW Protease.  
 SQ SEQUENCE 489 AA; 52664 MW; 01C2009712E3C76D CRC64;

Query Match 17.98; Score 178; DB 11; Length 489;  
 Best Local Similarity 28.68; Pred. No. 2.4e-08;  
 Matches 53; Conservative 25; Mismatches 73; Indels 34; Gaps 9;  
 QY 13 LDDDMREMTLHNGYRAAFARNYTSKRTWYDCTLEEKAYKSARK-----SEEPSE 68  
 DB 21 LTDEKQTMVLDLHNGYRAOVSP--PASDMLQHRWDELLAFAFAKAYQKCVGHKNGRGR 78  
 QY 69 EENVDFSAATINIPLEAGNSWSEIFELRGKYN-----KNGKTSNIAWMDSHDK 121  
 DB 79 GENLEAATIDEGMDVPLAVGN--WHEHE-----YNNSTATCDPNMCGHYTVWMSKTER 132  
 QY 122 LGCAVYDC-----SGKTH-VVCOYGPPEAKGDKTYEEGAPCSGSDYAGVYCDDDM 173  
 DB 133 ICGSHFCETLQGEVEMANHLVNCYEPGPNVNGRKRPYDGTGSCPCP---LGYSK----- 185  
 QY 174 ONLTC 178  
 DB 186 ENSLC 190

RESULT 21  
 ID 09NSN4 PRELIMINARY; PRT; 208 AA.  
 AC 09NSN4;  
 DT 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, last sequence update)  
 DT 01-JUN-2002 (Tremblrel. 21, last annotation update)

DE H10D18.4 protein.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Pseudocercariae; Caenorhabditis.  
 ON NCBI\_TaxID=6239;  
 RX MEDLINE=99069613; Pubmed=9851916;  
 RC STRAIN-BRISTOL N2;  
 RA None;  
 RT "Genome sequence of the nematode C. elegans: a platform for  
 RT investigating biology. The C. elegans Sequencing Consortium.";  
 RL Science 282:2012-2018(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RA Madsen C., Tin-Wollam A., Keppler D.;  
 RT "The sequence of C. elegans cosmid H10D18.";  
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RL Material R.;  
 DR EMBL: AC006655; LAF39876.1;  
 DR InterPro: IPR001283; Allrgn\_V5/Tpx1.  
 DR Pfam: PF00188; SCP.1.  
 DR PRINTS: PR00837; V5TPX1.  
 DR PRODOM: PD008342; Allrgn\_V5/Tpx1.1.  
 DR SMART: SM00198; SCP.1.  
 SQ SEQUENCE 208 AA; 22147 MW; 9FE6B3BE8A618BCF CRC64;  
 Query Match 16.8%; Score 167; DB 5; Length 208;  
 Best Local Similarity 26.8%; Pred. No. 8; 9e-08;  
 Matches 52; Conservative 22; Mismatches 58; Indels 62; Gaps 8;  
 QY 23 ELHNGYRAAFAR-NT-----TTSKRTMYDCTLEEKAKYSAKCSSE----- 64  
 DB 28 DAHNRKRSIAAGSSTVAAGTQEPASNMKRIWDETVAAAGAEACCPDHSGTSGEN 87  
 QY 65 -----PSSEENVDFSAATLNTIPLEAGNSMSEIFELRGVYNNKNTS----- 109  
 DB 88 LYSMSWSSAPSSSLDKRFVA-----ASNSWSE-----FKYGTSTFIDEAGFAT 132  
 QY 110 ---NINMNVWDSDHRLGCAVYDSCG-----KTHVCOYGPAPKAGDKITIEGAPCS 158  
 DB 133 GIGHATQAMAMETSKIGGICINCKANKKMYKVAVVCOTDSAGNMDSDIQSGETCS 192  
 QY 159 RCDYDAGVTCDD 172  
 DB 193 ACSE---DASCPD 203  
 RESULT 22  
 ORFCR8  
 ID ORFCR8 PRELIMINARY; PRT; 415 AA.  
 AC ORFCR8  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Hypothetical 45.2 kDa protein (Fragment).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 ON NCBI\_TaxID=9606;  
 RX MEDLINE=9606;  
 RC STRAIN-BRISTOL N2;  
 RA Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 RL EMBL: BC022399; AAH22399.1;  
 KW Hypothetical protein.

FT NON-TER 1 1  
 SQ SEQUENCE 415 AA; 45230 MW; 945069C1607D38E3 CRC64;  
 Query Match 15.9%; Score 159; DB 4; Length 415;  
 Best Local Similarity 28.6%; Pred. No. 1.2e-06;  
 Matches 53; Conservative 26; Mismatches 72; Indels 34; Gaps 9;  
 QY 13 LDDMEFTEHNGYRAAFARNTKTSKRTMYDCTLEEKAKYSAKCSSE----- 68  
 DB 35 LTDEKRLAVELHNTITRAOVSP--ASDMLHMDDELAFAKAYANOCVGHKNERGR 92  
 QY 69 ENVDVFSATLNTIPLEAGNSMSEIFELRGVYNNKNTSNIAM-----VDSHDR 121  
 DB 93 GENLPAITDEGNDVPL-AMEEMHE-----REHYNLSATCSPEQMGHYTOVYAKTER 146  
 QY 122 LCAVYDSCG-----KTHV--VCOYGPAPKAGDKITIEGAPCSRCDYDAGVTCDDW 173  
 DB 147 ICGSHFCKELGVEINTELVCNTEPPGNVKGKRPYQECTPCSCF--SGYHC--- 199  
 QY 174 QNLIC 178  
 DB 200 KNSLC 204  
 RESULT 23  
 Q9H336 PRELIMINARY; PRT; 500 AA.  
 ID Q9H336  
 AC Q9H336  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE Putative secretory protein precursor (Cococriasp).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 ON NCBI\_TaxID=9606;  
 RX MEDLINE=9606;  
 RC STRAIN-BRISTOL N2;  
 RA Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=HEART, AND TESTIS;  
 RA Smith D.M., Collins-Racie L.A., Lavallee E.R., Gamet L., Roberts D.J.,  
 RA Marigo V.A., Copeland N.G., Jenkins N.A., McCoy J., Tabin C.J.;  
 RT "A novel cysteine-rich secreted protein (CRISP) family member,  
 RT Cococriasp, provides insight into the process of septation in the  
 RT developing chicken midbrain.";  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=OVARY;  
 RA Strauberg R.;  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF142573; AAG43287.1;  
 DR EMBL: AF329197; AAK16495.1;  
 DR EMBL: BC020514; AAH20514.1;  
 DR HSP: P04284; ICPE.  
 DR InterPro: IPR001283; Allrgn\_V5/Tpx1.  
 DR InterPro: IPR004043; ICCL\_dcm.  
 DR Pfam: PF00188; SCP.1.  
 DR PRINTS: PR00837; V5TPX1.  
 DR PRODOM: PD008342; Allrgn\_V5/Tpx1.1.  
 DR SMART: SM00198; SCP.1.  
 DR PROSITE: PS01010; SCP\_NGS\_PRL-SC7.2.1.  
 SQ SEQUENCE 500 AA; 56888 MW; 203B1DC4DDA003CB CRC64;  
 Query Match 15.8%; Score 158; DB 4; Length 500;  
 Best Local Similarity 25.3%; Pred. No. 1.8e-06;  
 Matches 53; Conservative 31; Mismatches 66; Indels 58; Gaps 11;

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OY 1 EGDYSLCOOREK---LDDMKREMTLHNGYRAAFARNYKT-SKMTMYDCTLEKAYK 56
DB 43 DGMWYAKORGRATTDNDMSIL-DLHNKLR---SQYYPASMMWYMDVELERSAES 98
OY 57 SAKCSESE--PSSEENYDVFSATLNIPLLEAG-----NSWMSSEI----- 94
DB 99 MAESCIMEHGPPAS-----LLPSIGNLGAHNGRRPTFPVQSWYDEVDSYPRHEHC 152
OY 95 -----TELGRKYNNKGTSTNINMYWDSHDKLGAAYVDCSG-----KTHVCOY 139
DB 153 NPYCPRCGPV-----CTHYQYVWATSNIGAILCHNNNMIMQIMPKAVYLVCNY 205
OY 140 GPEAKGDGKTYIEGAPCSRC-SDYNG 166
DB 207 SPKGMWGHAPYKKGRCPSACPSFGG 234

RESULT 24
OQUB03 PRELIMINARY: PRT: 220 AA.
AC OQUB03:
DB 01-MAY-2000 (TREMBLrel. 13, Created)
DB 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DB 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DB Vespid allergen antigen homolog.
GN VAH.
OS Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidae;
OC Onchocercidae; Muchereria.
OC NCBI_TaxID=6293;
RN SEQUENCE FROM N.A.
RA Seltman A.K., Steel C.S., Ottesen E.A., Nutman T.B.;
RT Identification of potentially protective antigens in human lymphatic
RT filariasis.*;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DB EMBL; AF128091; AAD28256.1;
DR HSSP; P04284; ICPE.
DR InterPro; IPR001283; Allrgn_V5/TpX1.
DR Pfam; PF00188; SCP. 1.
DR PRINTS; PR00837; V5TPXLIKE.
DR PRODOM; PD000542; Allrgn_V5/TpX1; 1.
DR SMART; SM00198; SCP. 1.
SQ SEQUENCE 220 AA; 24617 MW; 7439F5DB1C96E978 CRC64;

Query Match 15.7%; Score 157; DB 5; Length 220;
Best Local Similarity 27.2%; Pred. No. 8, 2e-07;
Matches 50; Conservative 26; Mismatches 74; Indels 34; Gaps 10;

OY 12 KLDDDMREMTLHNGYRAAFARNY-----KTSKMTMYDCTLEKAYKSAK 61
DB 23 QLTPOQRKDIYRONNKRSLIRGLKNNGTYPGRKNMLQITWSCOLENSAORMNOC 82
OY 62 --SEEPSSE--ENDYV--SAATLNI-----PLEAGNSWSEIFELRGKYNNKGT 109
DB 83 VFGHSPKNOGIGENYVWSSAVENTLRKTACTENGKSWSELPETY-KHNSNNLTD 141
OY 110 NTA-----NMWDSHDKLGAAYVDC-SGKTRV-VCQYGPBAGDGKTYIEGAPCS 158
DB 142 DVSROGVLFHTOMAMGKTHKICGIAITNCDSGRTLITICHYSPAGNITLKNLYELGEPCK 201
OY 159 RQSD 162
DB 202 KDGD 205

RESULT 25
OQ7149 PRELIMINARY: PRT: 220 AA.
AC OQ7149:
DB 01-MAY-1999 (TREMBLrel. 10, Created)
DB 01-MAY-1999 (TREMBLrel. 10, Last sequence update)

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DB 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DB Vespid allergen antigen homolog.
GN VAH.
OS Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidae;
OC Onchocercidae; Muchereria.
OC NCBI_TaxID=6293;
RN SEQUENCE FROM N.A.
RA Hopkins R.M., McCarthy J.S.;
RT Cloning of the Muchereria bancrofti venom allergen homolog.*;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DB EMBL; AF108794; AAD16985.1;
DR HSSP; P04284; ICPE.
DR InterPro; IPR001283; Allrgn_V5/TpX1.
DR Pfam; PF00188; SCP. 1.
DR PRINTS; PR00837; V5TPXLIKE.
DR PRODOM; PD000542; Allrgn_V5/TpX1; 1.
DR SMART; SM00198; SCP. 1.
SQ SEQUENCE 220 AA; 24640 MW; 84314558E31540D4 CRC64;

Query Match 15.6%; Score 156; DB 5; Length 220;
Best Local Similarity 27.2%; Pred. No. 1e-06;
Matches 50; Conservative 26; Mismatches 74; Indels 34; Gaps 10;

OY 12 KLDDDMREMTLHNGYRAAFARNY-----KTSKMTMYDCTLEKAYKSAK 61
DB 23 QLTPOQRKDIYRONNKRSLIRGLKNNGTYPGRKNMLQITWSCOLENSAORMNOC 82
OY 62 --SEEPSSE--ENDYV--SAATLNI-----PLEAGNSWSEIFELRGKYNNKGT 109
DB 83 VFGHSPKNOGIGENYVWSSAVENTLRKTACTENGKSWSELPETY-KHNSNNLTD 141
OY 110 NTA-----NMWDSHDKLGAAYVDC-SGKTRV-VCQYGPBAGDGKTYIEGAPCS 158
DB 142 DVSROGVLFHTOMAMGKTHKICGIAITNCDSGRTLITICHYSPAGNITLKNLYELGEPCK 201
OY 159 RQSD 162
DB 202 KDGD 205

RESULT 26
OQ0608 PRELIMINARY: PRT: 207 AA.
AC OQ0608:
DB 01-NOV-1996 (TREMBLrel. 01, Created)
DB 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DB 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DB F99E11.9 protein.
GN F99E11.9.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
OC Rhabditidae; Felodertinae; Caenorhabditis.
OC NCBI_TaxID=6239;
RN SEQUENCE FROM N.A.
RA Baynes C.;
RT Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RL [2]
RN MEDLINE=99069613; PubMed=9851916;
RX none;
RA "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.*";
RL Science 283:2012-2018(1998).
DB EMBL; Z70308; CA94348.1;
DR InterPro; IPR001283; Allrgn_V5/TpX1.
DR Pfam; PF00188; SCP. 1.
DR PRINTS; PR00837; V5TPXLIKE.
DR PRODOM; PD000542; Allrgn_V5/TpX1; 1.
DR SMART; SM00198; SCP. 1.
SQ SEQUENCE 207 AA; 21932 MW; 5D6F6E96794B4C1A CRC64;

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Query Match      15.5%; Score 154.5; DB 5; Length 207;
Best Local Similarity 26.6%; Pred. No. 1.3e-06;
Matches 49; Conservative 19; Mismatches 71; Indels 45; Gaps 7;

QY 23 ELHNGYRAAFARNTKSK-----MRTWYDCTLEEKAYSAKCESEPSSE---70
DB 26 DANNKTRSAIAKSTYKAGKREKPEATDMKRMVSTVAASNOYAWTC---PTGHSKGTG 82
QY 71 -----NVDYFSAATLNIPLLEAGNSMSEIFELNGKYNK-----NGKTSNIAM 114
DB 83 YGENTYMTSADYGSIDSYG---ETAAAMKEKFODEGKMSNAMDITLFNSGIGHATQM 139
QY 115 VWDSDKRLGCAVVDSCS-----GTRHYCCYCGPEAKGDKTYEGAPCSRCSGDGAG 166
DB 140 AANAATSSIGCGVKNKGKGDASMRMNRKIAVCCYSPGNTGRTYREGTTCSSCS---GS 196
QY 167 VTCD 170
DB 197 TKCD 200

RESULT 27
Q93747 PRELIMINARY; PRT: 213 AA.
AC 093747;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DR 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
GN FAGE11.4 protein.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Telodermidae; Caenorhabditis.
OX NCBI_Taxid=6239;
RN (1)
RP SEQUENCE FROM N.A.
RA Baynes C.;
RL Submitted (MAR-1996) to the EMBL/Genbank/DBJ databases.
RX MEDLINE=99069613; PubMed=9851916;
RT none;
RT "Genome sequence of the nematode C. elegans: A platform for
investigating biology."
RL Science 282:2012-2018(1998).
EMBL; 270308; CA94349.1;
DR InterPro: IPR001283; Allrgn_V5/TpX1.
DR Pfam: PF00188; SCP: 1.
DR PRINTS: PR00837; VSTPLIKE.
DR PRODOM: PD000542; Allrgn_V5/TpX1.
DR SMART: SM00198; SCP: 1.
SQ SEQUENCE 213 AA; 23979 MW; ADD56E2B33A9D8A CRC64;

Query Match      15.3%; Score 153; DB 5; Length 213;
Best Local Similarity 27.1%; Pred. No. 1.8e-06;
Matches 45; Conservative 29; Mismatches 64; Indels 28; Gaps 7;

QY 24 LHNHYRAAR-----RMYKSKKRTWYDCTLEEKAYSAKCESEPS---SEEN 71
DB 31 VHNFEQSALQQLSFRGVKPKPSASMKRISMKRTJNAARFETCPKNSVYVANTGES 90
QY 72 VDVFSAAITNIPLE---AGNSMSEIFELRG---KYVNNKGTSNIAN---MYWDSHK 121
DB 91 ITHFSSISSTPEQATATAPQKMWNE-FETNGSDSLIYNHVSORFOIGHAVQMAHTTSK 149
QY 122 LGCAVVDSCGKTH-----VVCQYGEPAKGDGKTYEGAPCSRCS 162
DB 150 VGGGYSKCAVGTPEQTWVVCRCYFQKNGIEGPIYNEGETCTKPE 195

RESULT 28
Q20609

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ID Q20609 PRELIMINARY; PRT: 212 AA.
AC Q20609;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DR 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
GN FAGE11.5 protein.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Telodermidae; Caenorhabditis.
OX NCBI_Taxid=6239;
RN (1)
RP SEQUENCE FROM N.A.
RA Baynes C.;
RL Submitted (MAR-1996) to the EMBL/Genbank/DBJ databases.
RX MEDLINE=99069613; PubMed=9851916;
RT none;
RT "Genome sequence of the nematode C. elegans: A platform for
investigating biology."
RL Science 282:2012-2018(1998).
EMBL; 270308; CA94349.1;
DR InterPro: IPR001283; Allrgn_V5/TpX1.
DR Pfam: PF00188; SCP: 1.
DR PRINTS: PR00837; VSTPLIKE.
DR PRODOM: PD000542; Allrgn_V5/TpX1.
DR SMART: SM00198; SCP: 1.
SQ SEQUENCE 212 AA; 23359 MW; 5A4DB40539CB708C CRC64;

Query Match      15.2%; Score 152; DB 5; Length 212;
Best Local Similarity 24.5%; Pred. No. 2.3e-06;
Matches 51; Conservative 25; Mismatches 92; Indels 40; Gaps 8;

QY 4 YSLCOOREKLDDMEKMTLHNGYRAAR-----RMYKSKKRTWYDCTLEEK 54
DB 13 FSCFETLCFSETGANTYLSNHTLSQDLKRYVAGNSTPSPASNMKLLIMDTLET 72
QY 55 YKSAKCESEPSSEEND-----VFSAAITNIPLEAGNSMSEIFELRGKYNK 104
DB 73 QDYSTCPTGHSASRANGENRWMTSPVYTOTDAELLGNRSATLMSE-FOFG--WNG 129
QY 105 NGKTSNIAN-----MYWDSHKLGCAVVDSCGKTH-----VVCQYGEPAKGDGKTY 151
DB 130 NLTEELFNSGIGHATQMAATNKNKIGCISKCSDSDFGTQYVVCVSPAGNYIGMDY 189
QY 152 EGAAPCSRCSGDYGAAGVTCDDWQNLICI 179
DB 190 KSGETCSNCPD---GTNCES--STGLCV 212

RESULT 29
O16854 PRELIMINARY; PRT: 220 AA.
AC O16854;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DR 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
GN Activation-associated secreted protein-1.
OS Onchocerca volvulus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Onchocerca.
OX NCBI_Taxid=6282;
RN (1)
RP SEQUENCE FROM N.A.
RA SPRATIN-FORREST;
RL MEDLINE=20416487; PubMed=10960168;
RA Tave W.; Pearlin E.; Dimaech F.R.; Lustigman S.;
RT "Angiogenic activity of Onchocerca volvulus recombinant proteins
similar to vespid venom antigen 3."
RL Mol. Biochem. Parasitol. 109:91-99(2000).

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RE SEQUENCE FROM N.A.
RC STRAIN-F0RST.
RA Joseph G.T., Lustigman S.;
RT "Cloning and characterization of a cDNA clone, Ov B93 from a L3
RT library", (SEP-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF020586; BAB69625.2; -.
DR HSPB; P04284.1 CFE.
DR InterPro: IPR001283; Allrgn_V5/Tpx1.
DR Pfam: PF00188; SCP: 1.
DR PRINTS: PR00837; V5TPXLIKE.
DR ProDom: PD000542; Allrgn_V5/Tpx1; 1.
DR SMART: SM00198; SCP: 1.
DR PROSITE: PS01010; SCP_AGS_PRL_SG7.2; UNKNOWN_1.
SQ SEQUENCE 220 AA; 24510 MW; C089BFAE869EBAB CRC64;

Query Match 15.2%; Score 152; DB 5; Length 220;
Best Local Similarity 25.8%; Pred. No. 2.4e-06;
Matches 47; Conservative 24; Mismatches 69; Indels 42; Gaps 9;

OY 9 QREKLDMDREMFTEHNGCYRAAFARNY--KTSKMTWYVDCITLBEKAYKSAEC--SEE 64
DB 28 EKKKIVGQNNKYSDDLNGKLNKRGTYMPGKMLMELFMCKLSSAQRWANCICRHS 87
OY 65 PSSEENV--DVF-----SAATLNIPLENGSMWSEIFELRGKVKNGKTS 109
DB 88 PROEGEGENVYAVSSVVEGLKKTGCT---DAGKSWSKL---PLYENPNSSNN 138
OY 110 -----NIANNVWDSHDKLGCAV--VDCS--KTHVCOYGPPEAKGDKITVEGA 155
DB 139 MTKVAVAGVYLHTQANAKTKKICGVATGCGDGRLLVICHYPSGNMVGVIYTHRN 198
OY 156 PC 157
DB 199 PC 200

RESULT 30
OY2006 PRELIMINARY; PRT; 188 AA.
ID 092006;
AC 092006;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Late gestation lung protein 1.
GN LG1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MISTAR; TISSUE-LUNG;
RX MEDLINE-99292450; PubMed-10362728;
RA Kaplan F., Ledoux P., Kassamali F.Q., Gagnon S., Post M., Koehler D.,
RA Demling J., Swezey N.B.;
RT "A tumor developmentally regulated gene in lung mesenchyme: homology
RT to a novel developmentally regulated gene in lung mesenchyme: homology
RL Am. J. Physiol. 276:11027-11036(1999).
DR EMBL: AF109674; AAD16986.1; -.
DR HSPB; P04284.1 CFE.
DR InterPro: IPR001283; Allrgn_V5/Tpx1.
DR Pfam: PF00188; SCP: 1.
DR PRINTS: PR00837; V5TPXLIKE.
DR ProDom: PD000542; Allrgn_V5/Tpx1; 1.
DR SMART: SM00198; SCP: 1.
DR PROSITE: PS01010; SCP_AGS_PRL_SG7.2; 1.
SQ SEQUENCE 188 AA; 21907 MW; 5B6CC7515360BCE CRC64;

Query Match 14.8%; Score 148; DB 11; Length 188;
Best Local Similarity 26.9%; Pred. No. 4.6e-06;
Matches 52; Conservative 22; Mismatches 61; Indels 58; Gaps 11;

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OY 24 LHNGYRAAFARNY--KTSKMTWYVDCITLBEKAYKSAECSE--PSSEENVVPSAATL 80
DB 2 LHKLR-----GVYTPASMETWDELEERSAAAMQNCMEHCPAS-----LLVSGO 52
OY 81 NITLENG-----NSWSEIFELRGKYN-----KKGTSNIANNVW 116
DB 53 NLAVHMRGRSRGFWOSWIDEV-----KDYTPFHECNPCWPCSCGAMCTHTQWV 107
OY 117 DSHDKLGCAVYDC-----SGTHVCOYGPPEAKGDKITVEGAPCSR--SDYGA 165
DB 108 ATTNKIGCAVHTCRSMYSWYDINENAVYLWNTSPKGMWGEAPYRHRGRCSEPSSTYG 167
OY 166 GVTCDDDWQNLIC 178
DB 168 G--C-----RNNLC 174

RESULT 31
OY4932 PRELIMINARY; PRT; 220 AA.
ID 044932;
AC 044932;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Vespid allergen antigen homolog (Venom allergen antigen-like protein
DE 1).
OS Brugia malayi.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filariidae;
OC Onchocercidae; Brugia.
OX NCBI_Taxid=6279;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TRS LABS.
RA McCarthy J.S., Hopkins R.M.;
RT "Cloning of the Brugia malayi VA homolog";
RT Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RA Murray J., Gregory W.F., Almadja A.K., Maizels R.M.;
RT "Expression and immune recognition of Brugia malayi VAL-1, a homolog
RT of vespid venom allergens and Ancylostoma secreted proteins";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF042088; AAB97283.2; -.
DR EMBL: AF334661; AAK12274.1; -.
DR InterPro: IPR001283; Allrgn_V5/Tpx1.
DR Pfam: PF00188; SCP: 1.
DR PRINTS: PR00837; V5TPXLIKE.
DR ProDom: PD000542; Allrgn_V5/Tpx1; 1.
DR SMART: SM00198; SCP: 1.
SQ SEQUENCE 220 AA; 24761 MW; F22F11AD7768FE65 CRC64;

Query Match 14.8%; Score 148; DB 5; Length 220;
Best Local Similarity 29.4%; Pred. No. 5.6e-06;
Matches 45; Conservative 20; Mismatches 48; Indels 40; Gaps 10;

OY 41 MRMVWVDCITLBEKAYKSAEC--SEPSSE--ENVDF-----SAATLNIP 83
DB 62 MLIKSCLENSAQRANOCVGHSPRNRGIGENVYAVWSESEVKARNTACT----- 117
OY 84 LKNGSMWSEIFELRGKYN--NKGTSNIA-----NMVWDSHDKLGCAV--VDC-S 130
DB 118 -EAGKSMWSEL-----PKLYKQNSNNLTDVAVRQGVLFHTQWAGKTHKIGCAIATDCG 172
OY 131 GKTHV--VCOYGPPEAKGDKITVEGAPCSRCD 162
DB 173 GRTLIAICHYSPAGNMKLEIYELGEPCKTSD 205

RESULT 32
OY18543 PRELIMINARY; PRT; 208 AA.
ID 018543;
AC 018543;
DT 01-NOV-1996 (TREMBLrel. 01, Created)

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DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE C39E9.2 Protein.
GN C39E9.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Sams M.A.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C. elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; 270307; CA9435.1; -.
DR HSSP; P04284; ICFE.
DR InterPro; IPR001283; Allrgn_V5/Tpx1.
DR Pfam; PF00188; SCP; 1.
DR PRINTS; PR00837; V5TPX1KE.
DR ProDom; PD000542; Allrgn_V5/Tpx1; 1.
DR SMART; SM00198; SCP; 1.
SQ SEQUENCE 208 AA; 21928 MW; 3DAFBCB60C6C0E5 CRC64;

Query Match 14.7%; Score 146.5; DB 5; Length 208;
Best Local Similarity 24.3%; Pred. No. 7.2e-06;
Matches 45; Conservative 26; Mismatches 63; Indels 51; Gaps 7;

QY 24 LINGRAAFARNTYTSK-----MRTMYDCTLEEKAYKSAKESPESEENDV 64
DB 30 VHNTRSRNAGTYVAATLPIEAGNSMWSSEIFELRCGYVNNKNGKTSNIAN----- 89
QY 65 -----PSESEENDVESAATLPIEAGNSMWSSEIFELRCGYVNNKNGKTSNIAN----- 113
DB 90 LVMYWTSTNTNIDQFA-----TGSAMEKEFQDYG--WSSNTLSMSLFMTGIGHA 139
QY 114 --MWDSDHDLGCAVVDGS-----GKTHVVCYGPAPKADGKTYIEGAPCSRCSDYGA 165
DB 140 TCMMAAKTNLIGCGVKNCGKDTNGFNKYTVVCCYKPOGNTLNMONTITSGTCSKCP---S 196
QY 166 GVTCDD 170
DB 197 GTSCE 201

RESULT 33
Q9N3I3 PRELIMINARY; PRT; 246 AA.
ID Q9N3I3;
AC Q9N3I3;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical 26.9 kDa protein.
GN Y51H7C.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-BRISTOL N2;
RL MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN-BRISTOL N2;

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RA Bradshaw-Cordum H.; Dubugue T.;
RT "The sequence of C. elegans cosmid Y51H7C.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA STRAIN-BRISTOL N2;
RL Waterston R.;
RT "Direct Submission.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC024805; AAK3935.1; -.
DR InterPro; IPR001283; Allrgn_V5/Tpx1.
DR Pfam; PF00188; SCP; 1.
DR PRINTS; PR00837; V5TPX1KE.
DR ProDom; PD000542; Allrgn_V5/Tpx1; 1.
DR SMART; SM00198; SCP; 1.
KV Hypothetical protein.
SQ SEQUENCE 246 AA; 26913 MW; BID7D59DC07B399 CRC64;

Query Match 14.4%; Score 143.5; DB 5; Length 246;
Best Local Similarity 24.5%; Pred. No. 1.7e-05;
Matches 45; Conservative 24; Mismatches 68; Indels 47; Gaps 6;

QY 23 ELHNGRAAFARNTYTSK-----MRTMYDCTLEEKAYKSAKESPESEENDV 73
DB 29 DAHNEFRSSIAKGTVTYGLHAPATNIMKKMNTYIATAQNNANKCPKGDGPLEGVS 88
QY 74 -----VESAATLPIEAGNSMWSSEIFELRCGYVNNKNGKTSNIAN----- 113
DB 89 GECMSGSHINASGVNHLGAVAAKANSSE-----TYKKGMETDVMSPDFNSGVGHA 140
QY 114 --MWDSDHDLGCAVVDGSK-----THVVCYGPAPKADGKTYIEGAPCSRCSDYGA 166
DB 141 IIMTWYQVAVGCVKLCQKEDYQIAYVCKYWGQNGKINYESGPTCSACP--PN 197
QY 167 VTCD 170
DB 198 TTCD 201

RESULT 34
Q93746 PRELIMINARY; PRT; 207 AA.
ID Q93746;
AC Q93746;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE F49E11.6 protein.
GN F49E11.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Baynes C.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C. elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; 270308; CA94350.1; -.
DR HSSP; P04284; ICFE.
DR InterPro; IPR001283; Allrgn_V5/Tpx1.
DR Pfam; PF00188; SCP; 1.
DR PRINTS; PR00837; V5TPX1KE.
DR ProDom; PD000542; Allrgn_V5/Tpx1; 1.
DR SMART; SM00198; SCP; 1.
SQ SEQUENCE 207 AA; 22006 MW; 3072C43F25FEE626 CRC64;

Query Match 14.3%; Score 143; DB 5; Length 207;

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Best Local Similarity 23.0%; Pred. No. 1.5e-05;  
Matches 46; Conservative 24; Mismatches 62; Indels 68; Gaps 8;

QY 18 REMTEHLNGYRAAFARNTSK-----MTWVYCTLEKAYKSAEKSEPSSE 68  
DB 23 QOAVDAHNRKSSIKGYAKGTTOKSGSNMKTIMATVATSNQVANTC---PTGH 79  
QY 69 EE-----NVDVFAATLNIPLKGNWSMEITELGKTYMKNKTSN 110  
DB 80 SGGSGYENLYWYTSCTGTLNDFGPA-----ASSMSE-----FOYGTWISN 124  
QY 111 -----IANNVDSHDKLGCAYVDC-----GTHVYCOYGEAKGDKTI 150  
DB 125 TIDMNTFNGIGHATGMANMFAIGCGVKNCGKDPNSNGINAVYCCIKTPGYLNPPI 184  
QY 151 YEEGAPCSRSDYAGVATCD 170  
DB 185 YQGGTCAACP---SGTACD 201

RESULT 35  
QID 018540 PRELIMINARY; PRT; 210 AA.  
AC 018540; 1996 (TREMBLrel. 01, Created)  
DT 01-JUN-1998 (TREMBLrel. 05, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE C3989 6 protein.  
GN Caenorhabditis elegans.  
OS Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Pelodierinae; Caenorhabditis.  
NCBI\_TaxID=6239;  
DB [1]  
RP SEQUENCE FROM N.A.  
RA Submitted (MAR-1996) to the EMBL/Genbank/DBJ databases.  
RN [2]  
RX MEDLINE-99069613; PubMed-9851916;  
RA none;  
RT "Genome sequence of the nematode C. elegans: A platform for  
investigating biology.";  
RL Science 282:2012-2018 (1998).  
DB EMBL; 270307; CAA94332.1; .  
DR HSSP; P04284; ICPE.  
DR InterPro; IPR001283; Allrgn\_V5/TPx1.  
DR Pfam; PF00188; SCP; 1.  
DR PRINTS; PR00837; VSTPLIKE.  
DR ProDom; PD000542; Allrgn\_V5/TPx1. 1.  
DR SMART; SM00198; SCP; 1.  
SQ SEQUENCE 210 AA; 23030 MW; 06AEN89CD24DDE2F CRC64;

Query Match 14.2%; Score 142; DB 5; Length 210;  
Best Local Similarity 24.9%; Pred. No. 1.9e-05;  
Matches 48; Conservative 23; Mismatches 70; Indels 52; Gaps 8;

QY 18 REMTEHLNGYRAAFARNTSK-----MTWVYCTLEKAYKSAEKSEPSSE 68  
DB 23 KOSTLNHNDIRSRKAGYAKGNKRESATNMLKRWDSLEQSAQNTANGCHQHSIN 82  
QY 69 EENV-----DVFS-----AATLNIPLKGNWSMEITELGKTYMKNKTSN 105  
DB 83 DKTIGENLYWMSGDFSLDFGKINTVA-----WDHEFGQWMSNMKFSALTN 133  
QY 106 GRTSINAMWVDSHDKLGCAYVDCG-----KTHVYCOYGEAKGDKTIYEGAPC 157  
DB 134 TGVHAHQIAMAPTGIGGAYKNGCRDARKGGLFOVALVCOYRYVGNFFKNITNSGATC 193  
QY 158 SRCSYDYGAVTCD 170  
DB 194 SACP---AGTSC 203

RESULT 36  
QID 08WS91 PRELIMINARY; PRT; 117 AA.  
AC 08WS91;  
DT 01-MAR-2002 (TREMBLrel. 20, Created)  
DT 01-MAR-2002 (TREMBLrel. 15, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Putative esophageal gland cell secretory protein I3 (Fragment).  
GN HSP13.  
OS Heterodera glycines (Soybean cyst nematode).  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;  
OC Tylenchoidea; Heterodera; Heteroderinae; Heterodera.  
NCBI\_TaxID=51029;  
DB [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-21588107; PubMed-11730789;  
RA Gao B., Allen R., Maier T., Davis E.L., Baun T.J., Husey R.S.;  
RT "Molecular characterization and expression of two venom allergen-like  
protein genes in Heterodera glycines.";  
RL Int. J. Parasitol. 31:1617-1625 (2001).  
DB EMBL; AF343567; AAL73347.1; .  
DR InterPro; IPR001283; Allrgn\_V5/TPx1.  
DR InterPro; IPR001230; Prelyl\_site.  
DR Pfam; PF00188; SCP; 1.  
DR PRINTS; PR00837; VSTPLIKE.  
DR ProDom; PD000542; Allrgn\_V5/TPx1. 1.  
DR SMART; SM00198; SCP; 1.  
DR PROSITE; PS00294; PRENYLATION; UNKNOWN\_1.  
FT NON\_TER 1  
SQ SEQUENCE 117 AA; 12736 MW; 695F950ZCEI25D88 CRC64;

Query Match 14.1%; Score 141; DB 5; Length 117;  
Best Local Similarity 33.0%; Pred. No. 1.2e-05;  
Matches 32; Conservative 18; Mismatches 33; Indels 14; Gaps 5;

QY 85 ENGSWSSEI--TELKGY-----YKNKTSINIANWVDSHDKLGCAYVDC---SGRT 133  
DB 15 QACDMMAHEKQFQFSSLYLDMAQFNKG--IGHWSQAMASTAGICAMRCPSSWTMT 72  
QY 134 HVCQYGEAKGDKCTIYEGAPCSRSDYAGVATCD 170  
DB 73 WVCNKEAGNPLNPGYKKGAKSCSDYN-GATCD 108

RESULT 37  
QID 08WS93 PRELIMINARY; PRT; 208 AA.  
AC 08WS93;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE H10D18.2 protein.  
GN H10D18.2.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Pelodierinae; Caenorhabditis.  
NCBI\_TaxID=6239;  
DB [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN-BRISTOL N2;  
RX MEDLINE-99069613; PubMed-9851916;  
RA none;  
RT "Genome sequence of the nematode C. elegans: a platform for  
investigating biology. The C. elegans Sequencing Consortium.";  
RL Science 282:2012-2018 (1998).  
DB [2]  
RP SEQUENCE FROM N.A.  
RA STRAIN-BRISTOL N2;  
RA Maden C., Tin-Wollam A., Keppler D.;  
RT "The sequence of C. elegans cosmid H10D18.";  
RL Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.  
RN [3]

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RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL NZ;
RA Waterston R.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC006655; AAF39874.1;
DR InterPro: IPR001283; Allrgn_V5/TPx1.
DR Pfam: PF00188; SCP; 1.
DR PRINTS: PR00837; V5TPXLIKE.
DR ProDom: PD000542; Allrgn_V5/TPx1; 1.
DR SMART: SM00198; SCP; 1.
SO SEQUENCE 208 AA; 22470 MW; 917E04AD6C1DBF33 CRC64;

Query Match 14.1%; Score 141; DB 5; Length 208;
Best Local Similarity 24.0%; Pred. No. 2.4e-05;
Matches 43; Conservative 28; Mismatches 70; Indels 38; Gaps 8;

OY 25 HNGYRADA-RNY-----KTSKRTMYDCTLEEKAYSAKSCSEEPSEENVDF 75
DB 30 HNDLSATALGNDACTLEPPAANKRIKMDSTVASSAQYANTCPDHSSTGTGENLY 89
OY 76 SATATNP-----LEAGNSW-----VSEIFELRGVYNNKNGKTSNINAWYDSD 120
DB 90 WSMSSAFTSLDKFGVAASNSWEKEPDIYGEWSTY-HDADLPDSG--IGHATOMAKMETN 146
OY 121.KIGCAVYDCSG-----KTHVCCYGPBAKDGKTIYEAGAPGSCSDYAGYTCDD 171
DB 147.KIGCCGVKCKGDSNNMNTKVAAYCQDOAGNMDSITOSGDTCSFC--SSKCE 202

RESULT 38
OY 018347 PRELIMINARY; PRT; 221 AA.
DB 01-JAN-1998 (TEMBLrel. 05, Created)
DB 01-JAN-1998 (TEMBLrel. 05, Last sequence update)
DB 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE Venom allergen antigen 5-1ike protein.
GN NDIVA833.
OS Dirofilaria immitis (Canine heartworm).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Splirurida; Filarioidae;
OC Onchocercidae; Dirofilaria.
OX NCBI_TextID=6287;
RN [1]
RP SEQUENCE FROM N.A.
RA Tripp C.A.; Wisniewski N.;
RL "Dirofilaria immitis larval cDNA clone isolated with immune dog sera."
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF001100; AAB62535.1;
DR InterPro: IPR001283; Allrgn_V5/TPx1.
DR Pfam: PF00188; SCP; 1.
DR PRINTS: PR00837; V5TPXLIKE.
DR ProDom: PD000542; Allrgn_V5/TPx1; 1.
DR SMART: SM00198; SCP; 1.
DR ProSite: PS01010; SCP_AGS_PRI_SCT_2; UNKNOWN.1.
SO SEQUENCE 221 AA; 25158 MW; 5542B42B455046F7 CRC64;

Query Match 14.1%; Score 141; DB 5; Length 221;
Best Local Similarity 27.0%; Pred. No. 2.5e-05;
Matches 57; Conservative 17; Mismatches 65; Indels 72; Gaps 12;

OY 7 COORERLDDMREMTLHNGYRAAFARNY-----KTSKRTMYDCTLEEKAYK 56
DB 19 CEGGKLTPTERKNITQT-NKYSRLIRGKLKNDGYLMPGKMLMRRDCKLERKSON 77
OY 57 SAKKC---SEEPSEER---ENVDF-----SAATLNIPLEAGNSWSEIFELRG 99
DB 78 WANNCVFGRHPSSEERIGENVYAYVSSGVLDLKKTAGT-----DAGRLMSEL---E 128
OY 100 KVTN---KNGKTSNIA-----NMWDSHDKLCAVYDCSGKTR-----VYCO 138
DB 129 KYSDNPSNNLTSSEVAMENILHFTOMAGSEYKLG-----SGVDNIYIVAVATLWIFCH 182

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OY 139 YGPEAKDGKTIYEGAPC-----SRCS 161
DB 183 YFPGNMVYDLIELYELGNPCRNKDCRTKRC 213

RESULT 39
OY 018549 PRELIMINARY; PRT; 211 AA.
DB 01-NOV-1996 (TEMBLrel. 01, Created)
DB 01-NOV-1996 (TEMBLrel. 08, Last sequence update)
DB 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE F49E11.11 protein.
GN F49E11.11.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditidae; Rhabditoidae;
OC Rhabditidae; Rhabditinae; Caenorhabditis.
OX NCBI_TextID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Baynes C.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA MEDLINE-94150718; PubMed-7906398;
RA Wilson R.; Alnesough R.; Anderson K.; Baynes C.; Berks M.;
RA Bonfield J.; Burton J.; Connell M.; Copsey T.; Cooper A.;
RA Gratton M.; Dear S.; Du Z.; Durbin R.; Faveilo A.; Fulton L.;
RA Gardner A.; Green P.; Hawkins T.; Hillier L.; Jier M.; Johnston L.;
RA Jones M.; Kershaw J.; Kirsten N.; Laister N.; Latreille P.;
RA Lightning J.; Lloyd C.; McMurray A.; Mortimore B.; O'Callaghan M.;
RA Parsons J.; Percy C.; Rifkin L.; Roopra A.; Saunders D.; Showkeen R.;
RA Smaison N.; Smith A.; Sonhammer E.; Staden R.; Sulston J.;
RA Thierzy-Mieg J.; Thomas K.; Vaudin M.; Vaughan K.; Waterston R.;
RA Watson A.; Weinstock L.; Wilkinson-Sproat J.; Woldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RL Nature 368:32-38 (1994).
RN [3]
RP SEQUENCE FROM N.A.
RA Sims M.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z70308; CA94354.1;
DR EMBL: Z70307; CA94354.1; JOINED.
DR EMBL: Z70307; CA94354.1;
DR EMBL: Z70308; CA94354.1; JOINED.
DR HSSP: P04284; ICPE.
DR InterPro: IPR001283; Allrgn_V5/TPx1.
DR Pfam: PF00188; SCP; 1.
DR PRINTS: PR00837; V5TPXLIKE.
DR ProDom: PD000542; Allrgn_V5/TPx1; 1.
DR SMART: SM00198; SCP; 1.
DR ProSite: PS01010; SCP_AGS_PRI_SCT_2; UNKNOWN.1.
SO SEQUENCE 211 AA; 22676 MW; ADF90C8E263F58F2 CRC64;

Query Match 14.1%; Score 140.5; DB 5; Length 211;
Best Local Similarity 24.0%; Pred. No. 2.7e-05;
Matches 47; Conservative 25; Mismatches 71; Indels 53; Gaps 8;

OY 15 DDMREMTLHNGYRAAFARNYKSKMT-----WYDCTLEEKAYSAKSCSEEP 65
DB 22 ESTQOFTYDLHNLKRTSIAKGYVAKGTTRAGSNLLKMKWPTLATPAGTFAVTCRGH 81
OY 66 SEE---EN-----VDVFSATLNIPLEAGNSWSEIFELRGKYNNKNGKTSN 110
DB 82 SNAACVGENLYKMWSSLPFSGMDYIGG-----NASTVAMDEFOQTG--WTNNFTQA 131
OY 111 IAN-----NMWDSHDKLCAVYDCSGKTR-----GKTHVCCYGPBAKDGKTIYEG 154
DB 132 LANTGIGHANOMAMNTGLIGGVANKCPPELANNKRAVYVCOTKAGSNTLGGDITKSG 191
OY 155 APCSRCDYAGYTCDD 170

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DB 192 TTCACP---TGTTC 204

RESULT 40

OSQC035 PRELIMINARY: PRT: 332 AA.

AC 09C035: 01-JUN-2001 (TREMBlrel. 17, Created)

DF 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE 492150801IRIK protein.

GN 492150801IRIK.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RM (1)

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=TESTIS;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izaawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Glass C., King B., Kochiya H., Schiri L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.F., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbets P., Nozome P., Ring B., Ringwald M., Rodriguez S., Sakamoto N., Suzuki H., Togo-Oka K., Wang K.H., Weitz C., Whitaker C., Wilming L., Wyshak-Boris A., Yoshida K., Hasegawa I., Kawai H., Kohsaki S., Hayashizaki I., Functional annotation of a full-length mouse cDNA collection."

RA Nature 409:685-690(2001).

DR EMBL: AK014834; BAB29594.1; -

DR HSSP: P04284; ICFE.

DR MSG: MGI:1914787; 492150801IRIK.

DR InterPro: IPR001283; Allrgn\_V5/TpX1.

DR Pfam: PF00188; SCP: 1.

DR PRINTS: PR00837; V5TPX1IKE.

DR PRODOM: PD000542; Allrgn\_V5/TpX1; 1.

DR SMART: SM00198; SCP: 1.

SQ SEQUENCE 332 AA; 37784 MW; CEDBA2A0697FDDC CRC64;

Query Match 14.1%; Score 140.5; DB 11; Length 332;

Best Local Similarity 29.1%; Pred. No. 4.7e-05;

Matches 55; Conservative 20; Mismatches 67; Indels 47; Gaps 12;

DB 14 DDDREFFTELHNGYR-AAFAFNKTKSMRTMYDCTLEEKAYSAEKSEEPSSE----- 68

DB 47 DVDFINNEYVGLHNEELGTFPPGV---NLRFPMWDVALSRTFAAMGKKCMYSNHTLIDL 103

DB 69 EENDVFSATLNI---PLE-----AGNSWSEIFELGKAYN-----KNGKTSNIA 112

DB 104 HESHPVTEIGENMMWGPVEDEFTVTAIRSMHE-----KSYSLINDTCEDEONSHIT 158

DB 113 NMWDSHDKICAVYVDCS---GKTHV---VCOYGPAAKDGRTI---YEGAPRCSCD 162

DB 159 OLWVDSYKYGCAVYSCARAGFTHALPFCNAP-----GDTLRPRYAGGFCRCRC--- 211

DB 163 YGAGVTCDD 171

DB 212 -GPDQCTD 219

OSQC035 PRELIMINARY: PRT: 434 AA.

AC 09D2R3: 01-JUN-2001 (TREMBlrel. 17, Created)

DF 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE 1810049K24R1K protein.

GN 1810049K24R1K.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RM (1)

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=PANCREAS;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izaawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Glass C., King B., Kochiya H., Schiri L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.F., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbets P., Nozome P., Ring B., Ringwald M., Rodriguez S., Sakamoto N., Suzuki H., Togo-Oka K., Wang K.H., Weitz C., Whitaker C., Wilming L., Wyshak-Boris A., Yoshida K., Hasegawa I., Kawai H., Kohsaki S., Hayashizaki I., Functional annotation of a full-length mouse cDNA collection."

RA Nature 409:685-690(2001).

DR EMBL: AK019034; BAB31519.1; -

DR HSSP: P04284; ICFE.

DR MSG: MGI:1926142; 1810049K24R1K.

DR InterPro: IPR001283; Allrgn\_V5/TpX1.

DR InterPro: IPR004043; LCCL\_dom.

DR Pfam: PF00188; SCP: 1.

DR PRINTS: PR00837; V5TPX1IKE.

DR PRODOM: PD000542; Allrgn\_V5/TpX1; 1.

DR SMART: SM00198; SCP: 1.

DR PROSITE: PS01010; SCP\_AGS\_PRL\_SG7\_2; 1.

SQ SEQUENCE 434 AA; 48593 MW; CZ5067EB14647AC0 CRC64;

Query Match 14.0%; Score 140; DB 11; Length 434;

Best Local Similarity 25.8%; Pred. No. 7.2e-05;

Matches 48; Conservative 21; Mismatches 73; Indels 44; Gaps 8;

DB 24 LHNGRAFAFNRY-KTSKMTMYDCTLEEKAYSAEKSEEPSSEENDVFSATLNI 82

DB 2 LHNKLR---GVYPPASNMHEHWDDELERSAAMAHRCIMEHGP---AGILRSIGONT 54

DB 83 PLEAG-----NSWSEIFEL-----RGKYRNKNGKTSNIAANWVDSHDKLG 123

DB 55 AVHMGRTYSPGFHVQSYDEVKDYTYPRPHCTPRCRERSCGPMCTHYGVWVATTKIG 114

DB 124 CAVVDC-----SGKTHVCOYGPAAKDGRTI---YEGAPRCSCD 172

DB 115 CAVHCRMANWMDPTWENAVYLVCNTPSPKMWIGEARIKNGRCSCSCSGGCL----- 170

DB 173 WNTLC 178

DB 171 ---NLC 174

RESULT 42

OSQC035 PRELIMINARY: PRT: 262 AA.

AC 022421: 01-JUN-2001 (TREMBlrel. 17, Created)

DF 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE 1810049K24R1K protein.

GN 1810049K24R1K.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RM (1)

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=PANCREAS;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izaawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Glass C., King B., Kochiya H., Schiri L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.F., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Monbets P., Nozome P., Ring B., Ringwald M., Rodriguez S., Sakamoto N., Suzuki H., Togo-Oka K., Wang K.H., Weitz C., Whitaker C., Wilming L., Wyshak-Boris A., Yoshida K., Hasegawa I., Kawai H., Kohsaki S., Hayashizaki I., Functional annotation of a full-length mouse cDNA collection."

RA Nature 409:685-690(2001).

DR EMBL: AK019034; BAB31519.1; -

DR HSSP: P04284; ICFE.

DR MSG: MGI:1926142; 1810049K24R1K.

DR InterPro: IPR001283; Allrgn\_V5/TpX1.

DR InterPro: IPR004043; LCCL\_dom.

DR Pfam: PF00188; SCP: 1.

DR PRINTS: PR00837; V5TPX1IKE.

DR PRODOM: PD000542; Allrgn\_V5/TpX1; 1.

DR SMART: SM00198; SCP: 1.

DR PROSITE: PS01010; SCP\_AGS\_PRL\_SG7\_2; 1.

SQ SEQUENCE 434 AA; 48593 MW; CZ5067EB14647AC0 CRC64;

Query Match 14.0%; Score 140; DB 11; Length 434;

Best Local Similarity 25.8%; Pred. No. 7.2e-05;

Matches 48; Conservative 21; Mismatches 73; Indels 44; Gaps 8;

DB 24 LHNGRAFAFNRY-KTSKMTMYDCTLEEKAYSAEKSEEPSSEENDVFSATLNI 82

DB 2 LHNKLR---GVYPPASNMHEHWDDELERSAAMAHRCIMEHGP---AGILRSIGONT 54

DB 83 PLEAG-----NSWSEIFEL-----RGKYRNKNGKTSNIAANWVDSHDKLG 123

DB 55 AVHMGRTYSPGFHVQSYDEVKDYTYPRPHCTPRCRERSCGPMCTHYGVWVATTKIG 114

DB 124 CAVVDC-----SGKTHVCOYGPAAKDGRTI---YEGAPRCSCD 172

DB 115 CAVHCRMANWMDPTWENAVYLVCNTPSPKMWIGEARIKNGRCSCSCSGGCL----- 170

DB 173 WNTLC 178

DB 171 ---NLC 174

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DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
DE T12A7.3 protein.
GN T12A7.3
OC Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Kennard N.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE-99069613; PubMed-9851916;
RX none;
RT Genome sequence of the nematode C.elegans: A platform for
investigating biology.
RL Science 282:2012-2018(1998).
DR EMBL; 273911; CA98140.1; -.
DR InterPro; IPR001283; Allrgn_V5/7pxl.
DR InterPro; IPR002052; N6_Mtase.
DR Pfam; PF00188; SCP; 1.
DR ProDom; PD000542; Allrgn_V5/7pxl; 1.
DR SMART; SM00198; SCP; 1.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN.1.
SQ SEQUENCE 262 AA; 29919 MW; 1B51A10F5F603ABA CRC64;

Query Match 13.9%; Score 139; DB 5; Length 262;
Best Local Similarity 26.2%; Pred. No. 48-05;
Matches 59; Conservative 20; Mismatches 66; Indels 80; Gaps 11.

OY 14 DDDREMEFTE-----LHNGY-----RAAFARVYKT-----SKRTMYVDCIL 50
DB 59 DDEDEHEFMENEAFCDDNYCANNVYPRGSQLAG-NFYTKRTRKAAGSNIKKFTVNNAL 117
OY 51 EEKAYKAEKCEPSESEENVDVFSATLPILEAGNSW-----S 92
DB 118 ERSYISNOK--NFSQHS-----FTDISELFWHSTRREDNRKKGPAALH 163
OY 93 EIFELKRYVKNKGTSTNI-----ANNWDSHDKLCQAVDCS-----GKTH 134
DB 164 WIKFERKFWDSNITLNDLFSGVGHATQWADTYQMCVASHKEIKRTGRPTTKIC 223
OY 135 VVCOYGPEAKDGKTYIEGAPCSRCSDYAGVTCDDDMQNLICI 179
DB 224 VVCHYWKGNVLYNEPIYLEGPPCSKCE---SKKCDK--RTGLCI 262

RESULT 43
O18539 PRELIMINARY; PRT; 209 AA.
ID 018539
AC 018539;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-JAN-1998 (Tremblrel. 05, last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
DE C39E9.5 protein.
GN C39E9.5
OC Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Sims M.A.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE-99069613; PubMed-9851916;
RX none;
RT Genome sequence of the nematode C.elegans: A platform for
investigating biology.

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RL Science 282:2012-2018(1998).
DR EMBL; 270307; CA94331.1; -.
DR HSSP; P04284; 1CFE.
DR InterPro; IPR001283; Allrgn_V5/7pxl.
DR Pfam; PF00188; SCP; 1.
DR PRINTS; PR00837; V5TPXLIKE.
DR ProDom; PD000542; Allrgn_V5/7pxl; 1.
DR SMART; SM00198; SCP; 1.
SQ SEQUENCE 209 AA; 22319 MW; 50504B53A1DA67 CRC64;

Query Match 13.9%; Score 138.5; DB 5; Length 209;
Best Local Similarity 24.7%; Pred. No. 48-05;
Matches 46; Conservative 30; Mismatches 71; Indels 39; Gaps 7;

OY 18 REMFTLNGYRAAFARVYKTSK-----MRTVYDCTLEEKAYSAEKCEPSS 68
DB 23 KQNVNHNAAVRSSIAKGEVYAKGTRKDSATNMKMDNSLQSNQYANGCPMQHSPD 82
OY 69 EENVDFSAATLNIPL-----EAGNSWSEIFELRGKYNNKGTSTNIAN----- 113
DB 83 KSYGENTLFWAYSSPIITDLDKYQSAVDTVVSE-FQWFG--NNSNKEFTALMNTGIGHAT 139
OY 114 -MYWDSHDKLCQAVDC-----SGTHVVCQYGPEAKDGKTYIEGAPCSRCSDYG 164
DB 140 OVAMSTGQVCGAKKNGCADSVRGYKATVCOYKVPGNVLFKNINYSKACSAACP--- 196
OY 165 AGVTCO 170
DB 197 AGTSC 202

RESULT 44
O18538 PRELIMINARY; PRT; 209 AA.
ID 018538
AC 018538;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-JAN-1998 (Tremblrel. 05, last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
DE C39E9.4 protein.
GN C39E9.4
OC Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Sims M.A.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE-99069613; PubMed-9851916;
RX none;
RT Genome sequence of the nematode C.elegans: A platform for
investigating biology.
RL Science 282:2012-2018(1998).
DR EMBL; 270307; CA94330.1; -.
DR HSSP; P04284; 1CFE.
DR InterPro; IPR001283; Allrgn_V5/7pxl.
DR Pfam; PF00188; SCP; 1.
DR PRINTS; PR00837; V5TPXLIKE.
DR ProDom; PD000542; Allrgn_V5/7pxl; 1.
DR SMART; SM00198; SCP; 1.
SQ SEQUENCE 209 AA; 22459 MW; D9A915316027AFPA CRC64;

Query Match 13.8%; Score 137.5; DB 5; Length 209;
Best Local Similarity 24.3%; Pred. No. 58-05;
Matches 46; Conservative 21; Mismatches 75; Indels 47; Gaps 7;

OY 18 REMFTLNGYRAAFARVYKTSK-----SKRTMYVDCITLKKAYSAEKCS----- 62
DB 25 QOFTVLDHNSFRSLATGATYSINGTLKPAGSNIRKMSDSTLATSQTYANTCPTGFSNT 84
OY 63 -----EPPSSEENVDFSAATLNIPLKAGNSWSEIFELRGKYNNKNGK----- 107

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